

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:33:36 ; Search time 171 Seconds
(without alignments)
1637.512 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737

Sequence: 1 MSSARTPLPTLNEDTDEPT.....SGTSMAFKIASKINELKT 724

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980a:*
2: geneseqp1990a:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003ba:*
8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3737	100.0	724	ABU08527	Abu08527 Human ser
2	3737	100.0	724	ABR43964	Abx43964 Human ser
3	3737	100.0	724	AD130081	Adi30081 Human kin
4	3737	100.0	724	ADQ60236	Adq60236 Human kin
5	3736	100.0	724	AAE19051	Aae19051 Human PAR
6	3700.5	99.0	777	ABR43968	Abx43968 Human ser
7	3699	99.0	780	ABR43967	Abx43967 Human ser
8	3670.5	98.2	787	AD139619	Adj39619 Human cal
9	3654	97.8	722	ABR43965	Abx43965 Rat serin
10	3654	97.8	722	AD130083	Adi30083 Rat serin
11	3654	97.8	722	ADQ60238	Adq60238 Rat serin
12	3644	97.5	722	AAE88227	Aae88227 Rat neuro
13	3640	96.6	796	ABU11830	Abu11830 Human MDD
14	3589.5	96.1	799	AD140876	Adi40876 Human kin
15	3566	95.4	691	AAE19050	Aae19050 Human PAR
16	3564	95.4	691	ABR43966	Abx43966 Human ser
17	3555	95.1	804	AAW79333	Aaw79333 Human pro
18	3550.5	95.0	768	AAW78349	Aaw78349 Human pro
19	3515	94.1	745	AAE33550	Aae33550 Human mtc
20	3515	94.1	745	ABR43970	Abx43970 Human mtc
21	3515	94.1	745	ADG34768	Adg34768 Serine/ch
22	3515	94.1	745	ADG91722	Adg91722 Human ser
23	3515	94.1	745	ADL14100	Adl14100 Human mtc
24	3515	94.1	745	ADQ15058	Adq15058 Human can
25	3467	92.8	774	ABR43969	Abx43969 Serine/ch

ALIGNMENTS

26	3425	91.7	731	7	ADC99074	Adc99074 Human KPP
27	2555	68.4	793	7	ADC34764	Adc34764 Rat serin
28	2552	68.3	795	5	AAE19052	Aae19052 Human PAR
29	2552	68.3	795	5	AAE16258	Aae16258 Human kin
30	2552	68.3	795	8	ADQ88278	Adq88278 Human 138
31	2546	68.1	795	6	AAE33551	Aae33551 Human mtc
32	2546	68.1	795	7	ADG91723	Adg91723 Human mtc
33	2453	65.6	779	2	AAE98226	Aae98226 Rat neuro
34	2419.5	64.7	744	5	AAE19049	Aae19049 Human PAR
35	2414	64.6	737	8	AD140874	Adi40874 Human kin
36	2399.5	64.2	729	2	ABG73795	Abg73795 Murine MA
37	2399	64.2	729	2	AAW37158	Aaw37158 Human Twe
38	2399	64.2	729	4	AAE65628	Aae65628 Novel pro
39	2389	64.2	729	6	AAE33552	Aae33552 Human mtc
40	2389	64.2	729	7	ADC34765	Adc34765 Human C-T
41	2399	64.2	729	7	ADG91724	Adg91724 Human mtc
42	2399	64.2	729	8	AD129234	Adi129234 Human MAR
43	2399	64.2	729	8	AD129438	Adi129438 Human MAR
44	2395.5	64.1	776	7	ADG40427	Adg40427 Human MAR
45	2388	63.9	713	6	ABU07562	Abu07562 Human ser

RESULT 1
ID ABU08527 standard; protein; 724 AA.
XX

XX ABU08527;
XX

DT 30-MAY-2003 (first entry)
XX

DE Human serine/threonine protein kinase.
XX

KW Human; enzyme; serine/threonine protein kinase; chromosome 11;
XX

KM gene therapy.
XX

OS Homo sapiens.
XX

PN US6492156-B1.
XX

PD 10-DEC-2002.
XX

PF 31-OCT-2001; 2001US-00984890.
XX

PR 31-OCT-2001; 2001US-00984890.
XX

PA (PEKE) PE CORP NY.
XX

PI Yan C, Li Z, Neelam B, Difrancesco V, Beasley EM;
XX

DR WPI; 2003-327315/31.
XX

DR N-PSDB; ABX93647, ABX93648.
XX

PT Novel nucleic acid molecule encoding a kinase polypeptide related to
serine/threonine kinase subfamily; useful in development of human
therapeutics and diagnostic compositions.
XX

PS Claim 1; Fig 2; 107pp; English.
XX

XX The invention relates to an isolated nucleic acid molecule consisting of
comprising of a cDNA sequence or genomic sequence (appearing as ABX93647
and ABX93648) encoding a kinase polypeptide that is related to the
serine/threonine kinase subfamily, or their complements. Also included
are a nucleic acid vector comprising the nucleic acids and a host cell
containing the vector and used to produce the protein. The nucleic acids
are useful in treatment and for identifying a compound that can be used
to treat a disorder associated with nucleic acid expression of the kinase
gene, as query sequences to perform a search against sequence databases
(for e.g. identify other family members or related sequences), as primers
for PCR (to amplify any given region of a nucleic acid molecule), to
synthesize antisense molecules of desired length and sequences, for

CC constructing recombinant vectors, expressing antigenic portions of the
CC proteins, as probes for determining the chromosomal positions of the
CC nucleic acid molecules by in situ hybridisation, making vectors
CC containing the gene regulatory regions of the nucleic acid molecules,
CC designing ribozymes, constructing host cells expressing the nucleic
CC acids, and constructing transgenic animals. The nucleic acids are also
CC useful as hybridisation probes, and for drug screening to identify
CC compounds that modulate kinase nucleic acid expression (and to monitor
CC the effectiveness of the compounds). The gene for the kinase is located
CC on chromosome 11. The present sequence represents the human kinase of the
CC invention
CC
XX
SQ Sequence 724 AA:

Query Match 100.0%; Score 3737; DB 6; Length 724;
Best Local Similarity 100.0%; Pred. No. 5,4e-253;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSARTPLPTLNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
Db 1 MSSARTPLPTLNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
QY 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLFVIE 120
Db 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLFVIE 120
QY 121 TEKTLVLMVEYASGGVEFDYLVAHGMRKEKARAKRQVVSAYQCHQKFIYHRDIKAEN 180
Db 121 TEKTLVLMVEYASGGVEFDYLVAHGMRKEKARAKRQVVSAYQCHQKFIYHRDIKAEN 180
QY 181 LLLDADNMNIIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGEVDVWMSLGVTL 240
Db 181 LLLDADNMNIIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGEVDVWMSLGVTL 240
QY 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFILLNSKRGTLQIIMK 300
Db 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFILLNSKRGTLQIIMK 300
QY 301 DRMNQVGHEDDELKPYVEPLPDYKDPRTETLWVSMGTREBIODSLVGRYENWATYTL 360
Db 301 DRMNQVGHEDDELKPYVEPLPDYKDPRTETLWVSMGTREBIODSLVGRYENWATYTL 360
QY 361 LGYKSELESGDTITLTKRPSADLTNSAPSPSHKVQSVSNAPKORRFSDAQPAIPTSN 420
Db 361 LGYKSELESGDTITLTKRPSADLTNSAPSPSHKVQSVSNAPKORRFSDAQPAIPTSN 420
QY 421 SYSKKTQSNNAENKRPEDRESGRKASSTAKYPASPLPGLERKKTTPPSTMSVLTSTN 480
Db 421 SYSKKTQSNNAENKRPEDRESGRKASSTAKYPASPLPGLERKKTTPPSTMSVLTSTN 480
QY 481 RGRNSPLERASLQASISQNGKOSTAPORVPVAPSPAHNISSSGAPDRTPNPRGVSSRS 540
Db 481 RGRNSPLERASLQASISQNGKOSTAPORVPVAPSPAHNISSSGAPDRTPNPRGVSSRS 540
QY 541 TTHAGQLROVROOQNLPGVTVPASPSGHSQGRGASGSIFFSKFTSKFVRNINBESKOR 600
Db 541 TTHAGQLROVROOQNLPGVTVPASPSGHSQGRGASGSIFFSKFTSKFVRNINBESKOR 600
QY 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSKTTSSMEPNMGEIRKVLIDANSQ 660
Db 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSKTTSSMEPNMGEIRKVLIDANSQ 660
QY 661 SELHKRYMLLCHMGTPGHEDFVQWMEVCKLPRLSLNGVRFKRI9GTSMAFKNTASKIAN 720
Db 661 SELHKRYMLLCHMGTPGHEDFVQWMEVCKLPRLSLNGVRFKRI9GTSMAFKNTASKIAN 720
QY 721 ELKL 724
Db 721 ELKL 724

RESULT 2
ABR43964

ID ABR43964 standard; protein; 724 AA.
XX ABR43964;
AC
XX
DT 11-AUG-2003 (first entry)
XX
DE Human serine/threonine protein kinase 661_protcd.
XX
KW Serine/threonine protein kinase; cytosolic; antidiabetic; nootropic;
KW neuroprotective; antiinflammatory; analgesic; gene therapy; human;
KW chromosome 11q12-q13; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033708-A2.
XX
PD 24-APR-2003.
XX
PF 14-OCT-2002; 2002MO-EP011478.
XX
PR 15-OCT-2001; 2001US-0328804P.
PR 27-FEB-2002; 2002US-0359688P.
PR 01-JUL-2002; 2002US-0392365P.
PA (FARB) BAYER AG.
PI Koehler RH;
DR WPI; 2003-403226/38.
DR N-Psdb; ACC48080.
PT New polynucleotide encoding a serine/threonine protein kinase
PT polypeptide, useful for preventing, ameliorating or treating diseases
PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
PT a CNS disorder.
PS
XX
XX Claim 1; Page 138-141; 175dp; English.
XX
XX The invention relates to human serine/threonine protein kinase
XX polypeptide and encoding polynucleotides. The polypeptides can be
XX expressed by standard recombinant methodology. The polynucleotide and
XX polypeptide are useful in preventing, ameliorating or treating diseases
XX associated with serine/threonine protein kinase dysfunction. The diseases
XX include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
XX disease. These can also be used to treat pain associated with the above
XX disorders. The protein kinase is also used in various diagnostic assays
XX or in genetic testing. The present sequence represents a human serine/
XX threonine protein kinase 661_protcd
SQ Sequence 724 AA:

Query Match 100.0%; Score 3737; DB 6; Length 724;
Best Local Similarity 100.0%; Pred. No. 5,4e-253;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSARTPLPTLNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
Db 1 MSSARTPLPTLNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNRLKKTIG 60
QY 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLFVIE 120
Db 61 KGNFAKVKLARHILITGKEVAVKIIDKTQUNSSSLQQLFREVRIMKVLNPNIVKLFVIE 120
QY 121 TEKTLVLMVEYASGGVEFDYLVAHGMRKEKARAKRQVVSAYQCHQKFIYHRDIKAEN 180
Db 121 TEKTLVLMVEYASGGVEFDYLVAHGMRKEKARAKRQVVSAYQCHQKFIYHRDIKAEN 180
QY 181 LLLDADNMNIIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGEVDVWMSLGVTL 240
Db 181 LLLDADNMNIIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKKYDGEVDVWMSLGVTL 240
QY 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFILLNSKRGTLQIIMK 300
Db 241 YTLVSGSLPPDQGNLKELRERVLRGKYRIPFYMSDTCENLLKKFILLNSKRGTLQIIMK 300

Db	241	YTLVSGSLPFDGQNLKELRERVLRGKYRIPEYMTDCENLKKKFLILNPSKRGTLQIIMK	300	FT	Active-site	/note="Casein kinase II phosphorylation site"
Qy	301	DRMANNVGHEDDELKPYVEPLPDYKDPRTTLMNLSKGTREIODSLVGQRYNEVMATYLL	360	FT	/note="Serine/Threonine protein kinase active site"	171..183
Db	301	DRMANNVGHEDDELKPYVEPLPDYKDPRTTLMNLSKGTREIODSLVGQRYNEVMATYLL	360	FT	Modified-site	222..225
Qy	361	LGKXSELEGGDTTLTKRPSADLTNSAPSPSHKVORSVSAMPKORRFPDQAGPALPTSN	420	FT	Region	/note="Amidation site"
Db	361	LGKXSELEGGDTTLTKRPSADLTNSAPSPSHKVORSVSAMPKORRFPDQAGPALPTSN	420	FT	Modified-site	231..251
Qy	421	SYSKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNLSSTTN	480	FT	Modified-site	/note="Helix 1"
Db	421	SYSKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNLSSTTN	480	FT	Modified-site	275..278
Qy	481	RSNNSPLLERASLGGASLQNGKSTAPQRPVVASPSAHNLSGGAPDRNPFRCVSSRS	540	FT	Modified-site	/note="Casein kinase II phosphorylation site"
Db	481	RSNNSPLLERASLGGASLQNGKSTAPQRPVVASPSAHNLSGGAPDRNPFRCVSSRS	540	FT	Modified-site	290..292
Qy	541	TFHAGQLRQVRDOONLPYGVTPASPSGSGRRGASGISPKFTSPKVRNLNLPSSKDR	600	FT	Modified-site	/note="Protein kinase C phosphorylation site"
Db	541	TFHAGQLRQVRDOONLPYGVTPASPSGSGRRGASGISPKFTSKFVRNLNLPSSKDR	600	FT	Modified-site	291..294
Qy	601	VELTRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMRIRKYLIDANSCQ	660	FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"
Db	601	VELTRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMRIRKYLIDANSCQ	660	FT	Modified-site	338..341
Qy	661	SELHEKXMLCNGTQGHEDFVQWEMEVCLPRLSLNGVTFKRISGTSMVAFKNIASKIAN	720	FT	Modified-site	/note="Casein kinase II phosphorylation site"
Db	661	SELHEKXMLCNGTQGHEDFVQWEMEVCLPRLSLNGVTFKRISGTSMVAFKNIASKIAN	720	FT	Modified-site	348..353
Qy	721	ELKL 724		FT	Modified-site	/note="N-myristoylation site"
Db	721	ELKL 724		FT	Modified-site	366..369
RESULT 3						
AD130081						
ID	AD130081	standard; protein; 724 AA.				
AC	AD130081;					
XX	22-APR-2004	(first entry)				
DE		Human kinase protein.				
XX		Human; kinase; serine/threonine kinase; immune response; drug screening;				
KW		tissue typing; pharmacogenomic analysis; tumour;				
KW		brain anaplastic oligodendroglioma; lung carcinoma tissue;				
KW		soft tissue leiomyosarcoma; gene therapy; transgenic animal; cytostatic;				
KW		enzyme.				
OS		Homo sapiens.				
XX						
XX						
XX						
FT	Key	Location/Qualifiers				
FT	Modified-site	3..5				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	10..13				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	29..31				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	42..45				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	59..82				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	75..78				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	75..77				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	90..93				
FT	Modified-site	/note="N-glycosylation site"				
FT	Modified-site	121..123				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	133..136				
FT	Active-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	171..183				
FT	Modified-site	/note="Serine/Threonine protein kinase active site"				
FT	Modified-site	222..225				
FT	Region	/note="Amidation site"				
FT	Modified-site	231..251				
FT	Modified-site	/note="Helix 1"				
FT	Modified-site	275..278				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	290..292				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	291..294				
FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"				
FT	Modified-site	338..341				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	348..353				
FT	Modified-site	/note="N-myristoylation site"				
FT	Modified-site	366..369				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	374..376				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	385..388				
FT	Modified-site	/note="N-glycosylation site"				
FT	Modified-site	392..394				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	406..409				
FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"				
FT	Modified-site	423..425				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	442..445				
FT	Modified-site	/note="Amidation site"				
FT	Modified-site	442..444				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	444..447				
FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"				
FT	Modified-site	449..451				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	462..465				
FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"				
FT	Modified-site	479..481				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	480..483				
FT	Modified-site	/note="N-glycosylation site"				
FT	Modified-site	519..522				
FT	Modified-site	/note="N-glycosylation site"				
FT	Modified-site	537..539				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	559..564				
FT	Modified-site	/note="N-myristoylation site"				
FT	Modified-site	570..573				
FT	Modified-site	/note="Amidation site"				
FT	Modified-site	574..579				
FT	Modified-site	/note="N-myristoylation site"				
FT	Modified-site	584..586				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	603..605				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	610..615				
FT	Modified-site	/note="N-myristoylation site"				
FT	Modified-site	628..630				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	634..636				
FT	Modified-site	/note="Protein kinase C phosphorylation site"				
FT	Modified-site	639..642				
FT	Modified-site	/note="Casein kinase II phosphorylation site"				
FT	Modified-site	702..705				
FT	Modified-site	/note="cAMP- and cGMP-dependent protein kinase phosphorylation site"				
FT	Modified-site	706..711				

FT	/note= "N-myristoylation site"
Xn	
PX	US2003232408-A1.
PD	
XX	18-DEC-2003.
XX	
PF	21-OCT-2002; 2002US-00274194.
XX	
PR	31-OCT-2001; 2001US-00984890.
XX	
PA	(APPL-) APPLERA CORP.
PI	Yan C, Li Z, Neelam B, Difrancesco V, Beasley EM;
DR	WPI; 2004-061277/06.
N-P	N-P8DB; ADI30080, ADI30082.
xx	
PT	New peptides related to kinase protein subfamily useful for treating
PT	disorders associated with abnormal expression of kinase protein in
PT	testis, nervous tissue, fetal, lung, ovary tumor tissue.
xx	
PS	Claim 1; SEQ ID NO 2; 11pp; English.
xx	
CC	The invention relates to human kinase protein related to serine/threonine
CC	kinase subfamily and its corresponding nucleic acid sequence. The
CC	invention is useful to raise antibodies or to elicit immune response, as
CC	reagents in assays to determine the levels of protein in biological
CC	fluids, and as markers for tissues where the corresponding protein is
CC	expressed. It is also useful in drug screening assays, tissue typing and
CC	pharmacogenomic analysis. The sequences of the invention are useful in
CC	treating disorders associated with the absence of, inappropriate, or
CC	unwanted expression of kinase protein in testis, nervous tissue, foetal,
CC	lung, brain anaplastic oligodendroglioma, lung carcinoma tissue, soft,
CC	tissue leiomyosarcoma, ovary tumour tissue, or germ cell tumour tissue.
CC	These are also useful in gene therapy and are useful as models for the
CC	development of human therapeutic targets, aid in the identification of
CC	therapeutic proteins and serve as targets for the development of human
CC	therapeutic agents that modulate protease activity in cells and tissues
CC	that express the kinase peptide. The host cells are useful in producing a
CC	kinase protein or peptide, and non-human transgenic animals. The present
CC	sequence is human kinase protein.
xx	
SQ	Sequence 724 AA;
	Query Match 100.0%; Score 3737; DB 8; Length 724;
	Best Local Similarity 100.0%; Pred. No. 5,4e-253;
	Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 MSARPLPLTNERTEOPTGLHSDSRSSKSNMIRGNSATISADQPHIGNRLIKTTG 60
Dd	1 MSARTPLPLEINERTEOPTGLGHDSRSSKSNMIRGNSATSADQPHIGVRLIKTTG 60
Oy	61 KGNFARKVLARHIILGKEVAVKIIDKQLQNSSSLOKLFEVRIMTKVLNPNTVKLPEVIE 120
Dd	61 KGNFAKVKLARRHIILGKEVAVKIIDKQLQNSSSIQTLFRVRIIMTKVLNPNTVKLPEVIE 120
Oy	121 TEKTYILVWEVASGGEEVDYIVAHGRMKKEKAAPAKROVVSAYOYCHQKFIVHRDLKAEN 180
Dd	121 TEKTYILVWEVASGGEEVDYIVAHGRMKKEKAAPAKROVVSAYOYCHQKFIVHRDLKAEN 180
Oy	181 LLLDADNNIKITADRFSGNEFTPFGNKLDTPCGSPPYAAPLFQCKKYDGEVNVMSLGITL 240
Dd	181 LLLDADNNIKITADRFSGNEFTPFGNKLDTPCGSPPYAAPLFQCKKYDGEVNVMSLSGITL 240
Oy	241 YTVUSGSIPBPGQNLKELREKRVLRNGKTRIDFYNSTDCENILKKETLLNPSKRGTLEQIMK 300
Dd	241 YTVUSGSIPBFGQNLKELREKRVLRNGKTRIFPYNSTDCENILKKETLLNPSKRGTLEQIMK 300
Oy	301 DRMMNVGHEDEDELKPVEEPLPDYNDPRTETAMSMGYTREELODSLNGQRNYEWATYLL 360
Dd	301 DRMMNVGHEDEDELKPVEEPLPDYKDPRKTETAMSMGYTREELQDSLVGQRNYEWATYLL 360
Oy	361 LGYKSSSELBGDTTLTKRPESADLTINSAPSISHKVOVSANPKORRFSDAGPALPTSN 420

Db	361	LGTKSSLEEDTTLTPRPSADLTNSAPSPSHKVPQSVANPKQRFPDQAGPALPTSN	420
Qy	421	SYSKTQSNNAENKRPEDREDSGRKASSTAKVPASPLGLERKKTPTBSTNSVLSTSTN	480
Db	421	SYSKTQSNNAENKRPEDREDSGRKASSTAKVPASPLGLERKKTPTBSTNSVLSTSTN	480
Qy	481	RSNSPLLEBASIGQASIQNGKDSSTAPQVPVAPSPAHNIISSGGAPDRTNPFQGVSSRS	540
Db	481	RSNSPLLEBASIGQASIQNGKDSSTAPQVPVAPSPAHNIISSGGAPDRTNPFQGVSSRS	540
Qy	541	TFHAGQLQVRDQNLPGVTPASPBGHQGRGASGSIIFSFKTSTFVRNLNPEPSKOR	600
Db	541	TFHAGQLQVRDQNLPGVTPASPBGHQGRGASGSIIFSFKTSTFVRNLNPEPSKOR	600
Qy	601	VELTLRPHVVGSGGNDKEKEEPFPAKRSILFTWSMKTTSMEPNEMREIRKVLANSQ	660
Db	601	VELTLRPHVVGSGGNDKEKEEPFPAKRSILFTWSMKTTSMEPNEMREIRKVLANSQ	660
Qy	661	SELHEKXMLLCMHGTPGHEDFVQMEWEVCKLRLSLNGRFRRIIGTSMAFQNIASKIAN	720
Db	661	SELHEKXMLLCMHGTPGHEDFVQMEWEVCKLRLSLNGRFRRIIGTSMAFQNIASKIAN	720
Qy	721	EKL 724	
Db	721	EKL 724	
RESULT 4			
ADQ60236	ID	ADQ60236 standard; protein; 724 AA.	
XX	AC	ADQ60236;	
XX	DT	07-OCT-2004 (first entry)	
XX	DE	Human kinase.	
XX	KW	allelic variant; orthologue; therapeutic; kinase activity modulation;	
KW	KW	kinase associated disorder; human; kinase;	
XX	XX	serine/threonine kinase subfamily; enzyme.	
OS		Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	Region	3..5	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	10..13	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	29..31	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	42..45	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	59..82	
FT	Region	/note= "protein kinase ATP-binding region signature"	
FT	Region	75..78	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	75..77	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	90..93	
FT	Region	/note= "N-glycosylation site"	
FT	Region	121..123	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	133..136	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	222..225	
FT	Region	/note= "amidation site"	
FT	Region	275..278	
FT	Region	/note= "casein kinase II phosphorylation site"	
FT	Region	290..292	
FT	Region	/note= "protein kinase C phosphorylation site"	
FT	Region	291..294	
FT	Region	/note= "cAMP and cGMP dependent protein kinase	

FT phosphorylation site"
FT Region 338..341
FT /note= "casein kinase II phosphorylation site"
FT Region 348..353
FT /note= "N-myristoylation site"
FT Region 366..369
FT /note= "casein kinase II phosphorylation site"
FT Region 374..376
FT /note= "protein kinase C phosphorylation site"
FT Region 385..388
FT /note= "N-glycosylation site"
FT Region 392..394
FT /note= "protein kinase C phosphorylation site"
FT Region 406..409
FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Region 423..425
FT /note= "protein kinase C phosphorylation site"
FT Region 442..445
FT /note= "Amladation site"
FT Region 442..444
FT /note= "protein kinase C phosphorylation site"
FT Region 444..447
FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Region 449..451
FT /note= "protein kinase C phosphorylation site"
FT Region 462..465
FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Region 479..481
FT /note= "protein kinase C phosphorylation site"
FT Region 480..483
FT /note= "N-glycosylation site"
FT Region 519..522
FT /note= "N-glycosylation site"
FT Region 537..539
FT /note= "protein kinase C phosphorylation site"
FT Region 559..564
FT /note= "N-myristoylation site"
FT Region 570..573
FT /note= "Amladation site"
FT Region 574..579
FT /note= "N-myristoylation site"
FT Region 584..586
FT /note= "protein kinase C phosphorylation site"
FT Region 603..605
FT /note= "protein kinase C phosphorylation site"
FT Region 610..615
FT /note= "N-myristoylation site"
FT Region 628..630
FT /note= "protein kinase C phosphorylation site"
FT Region 634..636
FT /note= "protein kinase C phosphorylation site"
FT Region 639..642
FT /note= "casein kinase II phosphorylation site"
FT Region 702..705
FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Region 706..711
FT /note= "N-myristoylation site"
FT Region
XX US2004137499-A1.
XX 15-JUL-2004.
XX
XX 21-JAN-2004; 2004US-00760407.
XX
XX 31-OCT-2001; 2001US-00984890.
XX 21-OCT-2002; 2002US-00274194.
XX
XX (APPL-) APPLERA CORP.

PI Yan C, Li Z, Neelam B, DiFrancesco V, Beasley EM;
XX WPI; 2004-533359/51.
DR N-PSDB; ADO60235, ADO60237.
XX
PT New isolated human kinase peptide, useful for developing human
PT therapeutic targets, identifying therapeutic proteins, or as targets for
PT developing human therapeutic agents that modulate kinase activity in
PT cells and tissues.
XX
PS Claim 1; SEQ ID NO 2; 11np; English.
XX
CC The invention describes an isolated peptide (1). The peptide comprises an
CC amino acid sequence selected from: an amino acid sequence comprising 724
CC amino acids (SEQ ID NO. 2); an amino acid sequence of an allelic variant
CC of SEQ ID NO. 2, where the allelic variant is encoded by a nucleic acid
CC molecule that hybridizes to the opposite strand of a nucleic acid
CC molecule comprising 2175 bp (SEQ ID NO. 1) or 75395 bp (SEQ ID NO. 3); an
CC amino acid sequence of an orthologue of SEQ ID NO. 2, where the
CC orthologue is encoded by a nucleic acid molecule that hybridizes to the
CC opposite strand of SEQ ID NO. 1 or 3; or a fragment of SEQ ID NO. 2,
CC where the fragment comprises at least 10 contiguous amino acids. The
CC peptide sequence can be used as models for the development of human
CC therapeutic targets, aid in the identification of therapeutic proteins,
CC and serve as targets for the development of human therapeutic agents that
CC modulate kinase activity in cells and tissues and express the kinase.
CC They can also be used for biological assays related to kinases. In drug
CC screening assays in cell-based, or cell-free systems, it can also be used
CC to screen a compound for the ability to stimulate or inhibit interaction
CC between the kinase proteins and a molecule that normally interacts with
CC the kinase protein. They can also be used as targets for diagnosing a
CC disease or predisposition to disease mediated by the peptide, and for
CC treating disorders with an absence of, inappropriate, or unwanted
CC expression of the protein. This is the amino acid sequence of the human
CC kinase of the invention that is related to the serine/threonine kinase
CC subfamily.
XX
SQ Sequence 724 AA;

Query Match 100.0%; Score 3737; DB 8; Length 724;
Best Local Similarity 100.0%; Pred. No. 5,4e-253;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSARPTPLTINERDTPQPTLGHLDSPKSSKSMIRRNATGADBDPHIGNRLTLTG 60
DB 1 MSSARPPPLPTINRDRDTPQPTLGHLDSPKSSKSMIRRNATGADBDPHIGNRLTLTG 60

QY 61 KGNPAKYKLARHLITGKGVAVKTIIDKTQLNSSSLQKLFREVRIMKVANHPNIVLFEVIE 120
DB 61 KGNPAKYKLARHLITGKGVAVKTIIDKTQLNSSSLQKLFREVRIMKVANHPNIVLFEVIE 120

QY 121 TEKTLVLMVEYASGEVFDYLVAHGRMKEKARAKPQVAVQYCHQKFIVRDLKAEN 180
DB 121 TEKTLVLMVEYASGEVFDYLVAHGRMKEKARAKPQVAVQYCHQKFIVRDLKAEN 180

QY 181 LLDDADNNITKIDAPGNSNETFGNKLDTFGGSPPYAPBELFOGKTYGPEVDWVSLGVL 240
DB 181 LLDDADNNITKIDAPGNSNETFGNKLDTFGGSPPYAPBELFOGKTYGPEVDWVSLGVL 240

QY 241 YTLVSGSLPDPGONLKELRERVLRGKYRIPFYVSTDCENLKKFLLINPSKRGTLBOIMK 300
DB 241 YTLVSGSLPDPGONLKELRERVLRGKYRIPFYVSTDCENLKKFLLINPSKRGTLBOIMK 300

QY 301 DRMMNVGHEDEDELKPYVEPLPDYKDPRTTELAVSMGYTREBIQDSLGVGRYNEVMATYLL 360
DB 301 DRMMNVGHEDEDELKPYVEPLPDYKDPRTTELAVSMGYTREBIQDSLGVGRYNEVMATYLL 360

QY 361 LGYKSSLEBDTITTLKRPBADIITNSAPBPSHKVQSVANRQRRFSQAQAPATITSN 420
DB 361 LGYKSSLEBDTITTLKRPBADIITNSAPBPSHKVQSVANRQRRFSQAQAPATITSN 420

QY 421 SYSGKTSSNAENKRPDEDESGRKASSTAKVPASPLPGERKKTTTPTSTNSVLSTSTN 480
DB 421 SYSGKTSSNAENKRPDEDESGRKASSTAKVPASPLPGERKKTTTPTSTNSVLSTSTN 480

Db 421 SYSKKTQSNNAENKPEEDRESGRKASSTAKVPASPLPGLERKKTTPPTSTNSVLSTSTN 480
QY 481 RSRNSPLLERASLIGASIONGKDSAPORVPVSPASAHNISSSGGAPDRTNPPRGVSRS 540
Db 481 RSRNSPLLERASLIGASIONGKDSAPORVPVSPASAHNISSSGGAPDRTNPPRGVSRS 540
QY 541 TTHAOLQVPRROOQLPYGVTPASPSGHSQGRGASGSIFFSKFTSKFVRRLNDESKDR 600
Db 541 TTHAOLQVPRROOQLPYGVTPASPSGHSQGRGASGSIFFSKFTSKFVRRLNDESKDR 600
QY 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNMMEIRKVLDAWSCQ 660
Db 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNMMEIRKVLDAWSCQ 660
QY 661 SELHKRYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Db 661 SELHKRYMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
QY 721 ELKL 724
Db 721 ELKL 724

RESULT 5
AAE19051
ID AAE19051 standard; protein; 724 AA.
XX AC AAE19051;
DT 18-JUN-2002 (first entry)
XX DE Human PAR-1 β beta protein.
XX KM Human; Dishevelled associated kinase; PAR-1 kinase; enzyme; PAR-1 α ;
KW PAR-1 β alpha; PAR-1 β beta; PAR-1 γ ; cancer; hyperproliferative disease;
XX antisense therapy; Dsn.
OS Homo sapiens.
FH Key location/Qualifiers
FT Misc-difference 274 /note= "Encoded by AGG of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 275 /note= "Encoded by TGC of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 276 /note= "Encoded by CTG of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 277 /note= "Encoded by ACA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 278 /note= "Encoded by CTT of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 279 /note= "Encoded by TTG of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 280 /note= "Encoded by GAC of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 281 /note= "Encoded by GAA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 282 /note= "Encoded by TTC of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 283 /note= "Encoded by TTT of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 284 /note= "Encoded by AAA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "

FT Misc-difference 285 /note= "Encoded by GAG of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 286 /note= "Encoded by TAA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 287 /note= "Encoded by GAA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 288 /note= "Encoded by TTA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 289 /note= "Encoded by GGG of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 290 /note= "Encoded by TTC of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 291 /note= "Encoded by TCT of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 292 /note= "Encoded by TGC of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 293 /note= "Encoded by CCG of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 294 /note= "Encoded by TGA of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "
FT Misc-difference 295 /note= "Encoded by AAT of the inverse complementary
strand of the sequence shown as SEQ ID NO:8 (AAD33068) "

XX PN MO200210402-A2.
XX PD 07-FEB-2002.
XX PP 30-JUL-2001; 2001WO-US023981.
XX PR 28-JUL-2000; 2000US-0221860P.
XX PA (CHTR) CHIRON CORP.
XX PI Sun T, Feng J, Reinhard C, Fantl WJ, Williams LT;
XX DR MPI: 2002-206192/26.
XX PS N-PSDB; AAD30398; AAD33068.
XX FT Isolated nucleic acids encoding the human and Drosophila dishevelled
PT associated kinase, referred to as PAR-1 kinase, useful for identifying
PT modulators which can be used for modulating, inhibiting or preventing the
PT growth of cancer cells.
PS Claim 7, Page 286-288; 297pp; English.
XX The invention relates to Dishevelled (Dsh) associated kinase, referred to
CC as PAR-1 kinase in Drosophila and human homologues of PAR-1 referred to
CC as PAR-1 α , PAR-1 β (alpha and beta) and PAR-1 γ . The invention also
CC provides nucleic acid molecules encoding such proteins. PAR-1 activates
CC the Wnt pathway and is required for Wnt signalling in mammalian cells.
CC The PAR-1 modulators can be used to reduce the expression and/or
CC biological activity of PAR-1. They are useful for modulating, inhibiting
CC or preventing the growth of cancer cells. They are also useful for
CC treating other diseases of hyperproliferation. Sequences of the invention
CC are used in antisense therapy. The present sequence is human PAR-1 β beta
XX protein
XX SQ Sequence 724 AA;

QY Query Match 100.0%; Score 3736; DB 5; Length 724;
Best Local Similarity 99.9%; Pred. NO. 6.3e-253;
Matches 723; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 MSARFPLPTLNERDQPTLGHLSKPSKSNMIRNSATSADQPHIGNYRLTKTIG 60
|||||

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Db      1  MSARPTPLPTLNERTDEQPTLGHLDSPKSSKSNMIRGNRSATSADEQPHIGNYLLKTIG 60
Qy      61  KGNPAKYKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIYVLFEVIE 120
Db      61  KGNPAKYKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIYVLFEVIE 120
Qy      121  TEKTLVYVMEYASGGEVFDYLVAGRMKEKARAKFRQVVASVOYCHOKFIYHDLKAEN 180
Db      121  TEKTLVYVMEYASGGEVFDYLVAGRMKEKARAKFRQVVASVOYCHOKFIYHDLKAEN 180
Qy      181  LLLDADNMNIKIADFGFSENEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGEVDVMSLGVIL 240
Db      181  LLLDADNMNIKIADFGFSENEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGEVDVMSLGVIL 240
Qy      241  YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSSTDCENLLKKFLINPSKRGTLQIOMK 300
Db      241  YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSSTDCENLLKKFLINPSKRGTLQIOMK 300
Qy      301  DRMMNVGHEDDELKPYVEPLPDYKDPRTTELVMGTYRREIIDLVLGQRYNEVMATYLL 360
Db      301  DRMMNVGHEDDELKPYVEPLPDYKDPRTTELVMGTYRREIIDLVLGQRYNEVMATYLL 360
Qy      361  LGYKSSLEBDITTLKRPSPADLTNNSAPSPSHKVQSVSANPKQRRFSDQAPALPTSN 420
Db      361  LGYKSSLEBDITTLKRPSPADLTNNSAPSPSHKVQSVSANPKQRRFSDQAPALPTSN 420
Qy      421  SYSKKTQSNNAEKRPREDRESGRKASTAKVPSPLPGLERKKTPTPTSTNSVLSTSTN 480
Db      421  SYSKKTQSNNAEKRPREDRESGRKASTAKVPSPLPGLERKKTPTPTSTNSVLSTSTN 480
Qy      481  RSRNSPLLERASLGQASIQNGKSDTAPORVVASPSAMNISSSGADRTNFPGVSSRS 540
Db      481  RSRNSPLLERASLGQASIQNGKSDTAPORVVASPSAMNISSSGADRTNFPGVSSRS 540
Qy      541  TFHAGQLRQVRDQNLPEYVTPASPSGHSQGRGASGISFKTSTKFRRLNLPESKDR 600
Db      541  TFHAGQLRQVRDQNLPEYVTPASPSGHSQGRGASGISFKTSTKFRRLNLPESKDR 600
Qy      601  VETLRPRVVGSGGNDKEKEFREAKPRSLRPTWSMKTSSMEPEMMAREIRKVLDA NSCQ 660
Db      601  VETLRPRVVGSGGNDKEKEFREAKPRSLRPTWSMKTSSMEPEMMAREIRKVLDA NSCQ 660
Qy      661  SELHEKMLTLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIAS KIAN 720
Db      661  SELHEKMLTLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIAS KIAN 720
Qy      721  ELKYL 724
Db      721  ELKYL 724
RESULT 6
ABR43968 ID ABR43968 standard; protein; 777 AA.
XX      XX ABR43968;
XX      XX
XX      XX 11-AUG-2003 (first entry)
XX      XX
XX      XX Human serine/threonine protein kinase.
XX      XX
XX      XX Serine/threonine protein kinase; cytosolic; antidiabetic; nootropic;
XX      XX neuroprotective; antiinflammatory; analgesic; gene therapy; human;
XX      XX chromosome 11q12-q13; enzyme.
XX      XX
XX      XX Homo sapiens.
XX      XX
XX      XX Key Location/Qualifiers
XX      XX
XX      XX MISC-difference 558 /note= "the corresponding DNA encodes a residue which is
XX      XX not indicated in the present sequence"
XX      XX
XX      XX MO2003033708-A2.
```

```
XX      XX 24-Apr-2003.
XX      XX
XX      XX 14-OCT-2002; 2002W0-EP011478.
XX      XX
XX      XX 15-OCT-2001; 2001US-0328804P.
XX      XX 27-FEB-2002; 2002US-0359688P.
XX      XX 01-JUL-2002; 2002US-0392365P.
XX      XX
XX      XX (FARB ) BAYER AG.
XX      XX
XX      XX Koehler RH;
XX      XX
XX      XX WPI: 2003-403226/38.
XX      XX N-PSDB; ACC48106.
XX      XX
XX      XX New polynucleotide encoding a serine/threonine protein kinase
XX      XX polypeptide, useful for preventing, ameliorating or treating diseases
XX      XX associated with the protein kinase dysfunction, e.g. cancer, diabetes or
XX      XX a CNS disorder.
XX      XX
XX      XX Example 2; Page 167-169; 175pp; English.
XX      XX
XX      XX The invention relates to human serine/threonine protein kinase
XX      XX polypeptide and encoding polynucleotides. The polypeptides can be
XX      XX expressed by standard recombinant methodology. The polynucleotide and
XX      XX polypeptide are useful in preventing, ameliorating or treating diseases
XX      XX associated with serine/threonine protein kinase dysfunction. The diseases
XX      XX include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
XX      XX disease. These can also be used to treat pain associated with the above
XX      XX disorders. The protein kinase is also used in various diagnostic assays
XX      XX or in genetic testing. The present sequence represents a human serine/
XX      XX threonine protein kinase
XX      XX
XX      XX Sequence 777 AA;
XX      XX
XX      XX Query Match 99.0%; Score 3700.5; DB 6; Length 777;
XX      XX Best Local Similarity 93.2%; Pred. No. 2.2e-250;
XX      XX Matches 724; Conservative 0; Mismatches 0; Indels 53; Gaps 1;
Qy      1  MSARPTPLPTLNERTDEQPTLGHLDSPKSSKSNMIRGNRSATSADEQPHIGNYLLKTIG 60
Db      1  MSARPTPLPTLNERTDEQPTLGHLDSPKSSKSNMIRGNRSATSADEQPHIGNYLLKTIG 60
Qy      61  KGNPAKYKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIYVLFEVIE 120
Db      61  KGNPAKYKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIYVLFEVIE 120
Qy      121  TEKTLVYVMEYASGGEVFDYLVAGRMKEKARAKFRQVVASVOYCHOKFIYHDLKAEN 180
Db      121  TEKTLVYVMEYASGGEVFDYLVAGRMKEKARAKFRQVVASVOYCHOKFIYHDLKAEN 180
Qy      181  LLLDADNMNIKIADFGFSENEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGEVDVMSLGVIL 240
Db      181  LLLDADNMNIKIADFGFSENEFTFGNKLDTFCGSPPYAAPLPEFGKKYDGEVDVMSLGVIL 240
Qy      241  YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSSTDCENLLKKFLINPSKRGTLQIOMK 300
Db      241  YTLVSGSLPPDGOQLKELRERVLRGKYRIPFYMSSTDCENLLKKFLINPSKRGTLQIOMK 300
Qy      301  DRMMNVGHEDDELKPYVEPLPDYKDPRTTELVMGTYRREIIDLVLGQRYNEVMATYLL 360
Db      301  DRMMNVGHEDDELKPYVEPLPDYKDPRTTELVMGTYRREIIDLVLGQRYNEVMATYLL 360
Qy      361  LGYKSSLEBDITTLKRPSPADLTNNSAPSPSHKVQSVSANPKQRRFSDQAPALPTSN 420
Db      361  LGYKSSLEBDITTLKRPSPADLTNNSAPSPSHKVQSVSANPKQRRFSDQAPALPTSN 420
Qy      421  SYSKKTQSNNAEKRPREDRESGRKASTAKVPSPLPGLERKKTPTPTSTNSVLSTSTN 480
Db      421  SYSKKTQSNNAEKRPREDRESGRKASTAKVPSPLPGLERKKTPTPTSTNSVLSTSTN 480
Qy      481  RSRNSPLLERASLGQASIQNGKSDTAPORVVASPSAMNISSSGADRTNFPGVSSRS 540
Db      481  RSRNSPLLERASLGQASIQNGKSDTAPORVVASPSAMNISSSGADRTNFPGVSSRS 540
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Db      481 RSRNSPLERASLGGASLQNGKDSLTMPSRSTASASAAVSARPRQHKMSASVHPN 540
Qy      505 -----TAPORVPVAPSAHNISSSGGAPDRTNPPRGVSSRSTFHAQL 547
Db      541 KASGLPPTESNCEVPRPTAPQRPVAPSAHNISSSGGAPDRTPNPPRGVSSRSTFHAQL 600
Qy      548 RQVRDQONLPYGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETLAPH 607
Db      601 RQVRDQONLPYGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETLAPH 660
Qy      608 VVSGSGNDKEKEEFREAKRSLRFTWSMKTTSMEPNEMREIRKVLNANSCOSELHXY 667
Db      661 VVSGSGNDKEKEEFREAKRSLRFTWSMKTTSMEPNEMREIRKVLNANSCOSELHXY 720
Qy      668 MLLCMHGTPGHEDPVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db      721 MLLCMHGTPGHEDPVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 777

```

RESULT 7

ABR43967
ID ABR43967 standard; protein; 780 AA.

AC ABR43967;

DT 11-AUG-2003 (first entry)

DE Human serine/threonine protein kinase.

KW Serine/threonine protein kinase; cytosolic; antidiabetic; nootropic;
KW neuroprotective; antiinflammatory; analgesic; gene therapy; human;
KW chromosome 11q12-q13; enzyme.

OS Homo sapiens.

XX MO200303708-A2.

XX PN 24-APR-2003.

XX PF 14-OCT-2002; 2002WO-EP011478.

XX PR 15-OCT-2001; 2001US-0328804P.

XX PR 27-FEB-2002; 2002US-0356888P.

XX PR 01-JUL-2002; 2002US-0392365P.

XX PA (FARB) BAYER AG.

XX PI Koehler RH;

XX DR WPI: 2003-403226/38.

XX DR N-PSDB; ACC48105.

XX PT New polynucleotide encoding a serine/threonine protein kinase
XX PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
XX PT a CNS disorder.

PS Claim 1, Page 163-165; 175pp; English.

XX CC The invention relates to human serine/threonine protein kinase
XX CC polypeptide and encoding polynucleotide. The polypeptides can be
XX CC expressed by standard recombinant methodology. The polynucleotide and
XX CC polypeptide are useful in preventing, ameliorating or treating diseases
XX CC associated with serine/threonine protein kinase dysfunction. The diseases
XX CC include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
XX CC disease. These can also be used to treat pain associated with the above
XX CC disorders. The protein kinase is also used in various diagnostic assays
XX CC or in genetic testing. The present sequence represents a human serine/
XX CC threonine protein kinase
SO Sequence 780 AA;

Query Match 99.0%; Score 3699; DB 6; Length 780;
Best Local Similarity 92.8%; Pred. No. 2,8e-250;
Matches 724; Conservative 0; Mismatches 0; Indels 56; Gaps 1;

```

Qy      1 MSSARPTPLTNRDPEOPLTGLHDSKPSKSNMTRGRNSATSDBOPIHNYRLIKTTG 60
Db      1 MSSARPTPLTNRDPEOPLTGLHDSKPSKSNMTRGRNSATSDBOPIHNYRLIKTTG 60
Qy      61 KGNFAVKLARHILNTEKEVAVKIIDKTQNSSSLQCLFREVAIMKVLNPNIVKLFEVIE 120
Db      61 KGNFAVKLARHILNTEKEVAVKIIDKTQNSSSLQCLFREVAIMKVLNPNIVKLFEVIE 120
Qy      121 TEKTLVLNMEYASGGVFYTLVAHGMEKEKRAKFRQVSAVQCHQKFIYHDLKAEN 180
Db      121 TEKTLVLNMEYASGGVFYTLVAHGMEKEKRAKFRQVSAVQCHQKFIYHDLKAEN 180
Qy      181 ILLADAMNIIKIDPFGSNFTFGNKLDPFCGSPYAAAPBLPGKKYDDEVDVMSLGVTL 240
Db      181 ILLADAMNIIKIDPFGSNFTFGNKLDPFCGSPYAAAPBLPGKKYDDEVDVMSLGVTL 240
Qy      241 YTLVSGSLPFDGQNLKELEERVLRGKYRIPFYMSIDCENLLKKFLILNPSKRGTLQIMK 300
Db      241 YTLVSGSLPFDGQNLKELEERVLRGKYRIPFYMSIDCENLLKKFLILNPSKRGTLQIMK 300
Qy      301 DRMMNVGHEDDELKPYVEPLPYKDPRTTELMVSGYTRBEI QDSLVCQRNVEWATYLL 360
Db      301 DRMMNVGHEDDELKPYVEPLPYKDPRTTELMVSGYTRBEI QDSLVCQRNVEWATYLL 360
Qy      361 LGYKSELEGDITTLKPRPSADLTNSAPSPSHKQSVSANPQORRPSDQAGALPTSN 420
Db      361 LGYKSELEGDITTLKPRPSADLTNSAPSPSHKQSVSANPQORRPSDQAGALPTSN 420
Qy      421 SYSKKTQSNMANKRPEEDRESGRKASTAKVAPSLPGLERKKTTPPTSTNSVLSSTGN 480
Db      421 SYSKKTQSNMANKRPEEDRESGRKASTAKVAPSLPGLERKKTTPPTSTNSVLSSTGN 480
Qy      481 RSRNSPLERASLGGASLQNGKDSLTMPSRSTASASAAVSARPRQHKMSASVHPN 540
Db      481 RSRNSPLERASLGGASLQNGKDSLTMPSRSTASASAAVSARPRQHKMSASVHPN 540
Qy      505 -----TAPORVPVAPSAHNISSSGGAPDRTNPPRGVSSRSTFHA 544
Db      541 KASGLPPTESNCEVPRPTAPQRPVAPSAHNISSSGGAPDRTNPPRGVSSRSTFHA 600
Qy      545 GOLRQVRDQONLPYGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETL 604
Db      601 GOLRQVRDQONLPYGVTPASPSPGSHQGRGASGSI FSKFTSKFYRRNLNBPESKDRVETL 660
Qy      605 RPHVVGSGNDKEKEEFREAKRSLRFTWSMKTTSMEPNEMREIRKVLNANSCOSELH 664
Db      661 RPHVVGSGNDKEKEEFREAKRSLRFTWSMKTTSMEPNEMREIRKVLNANSCOSELH 720
Qy      665 EKMVLLCMHGTPGHEDPVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db      721 EKMVLLCMHGTPGHEDPVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 780

```

RESULT 8

ADJ96619
ID ADJ96619 standard; protein; 787 AA.

AC ADJ96619;

DT 06-MAY-2004 (first entry)

DE Human calcium/calmodulin-dependent protein kinase MARK2 protein Segid 76.

XX CC kinase; human; SNP; single nucleotide polymorphism;
XX CC cytosine protein kinase; serine/threonine protein kinase; PKC; SNK;
XX CC gene therapy; cancer; immune-related disease; cardiovascular disease;
XX CC brain; neuronal associated disease; metabolic; inflammatory disorder;
XX CC cytosolic; neuroprotective; immunomodulator; antiinflammatory; enzyme;
XX CC calcium/calmodulin-dependent protein kinase; MARK2.


```

XX OS Homo sapiens.
XX 72.
XX Key Location/Qualifiers
XX FT Misc-difference 415
XX FT /note= "Wild type Ala substituted for Pro by single
XX FT nucleotide polymorphism"
XX
XX MO2004006838-A2.
XX
XX PD 22-JAN-2004.
XX
XX PE 15-JUL-2003; 2003WO-US021730.
XX
XX PR 15-JUL-2002; 2002US-0395632P.
XX
XX PA (BUGE-) SUGEN INC.
XX
XX PI Whyte D, Manning G, Caenepeel S;
XX
XX DR WPI; 2004-122753/12.
XX
XX DR N-PSDB; ADJ96553.
XX
XX PT New nucleic acid molecule encoding a kinase polypeptide, useful for
XX PT preparing a composition for treating diseases or disorders, e.g., cancer,
XX PT or neurological, immunological or inflammatory disorders.
XX
XX PS Claim 1; SEQ ID NO 76; 366bp; English.
XX
XX CC This invention relates to a novel isolated, enriched or purified nucleic
XX CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
XX CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
XX CC as well as protein kinase-like enzymes. The present invention describes
XX CC screening methods to identify agonists, antagonists and antibodies that
XX CC can be used to modulate the activity or function of the mammalian kinase
XX CC enzymes. As such, these compositions can be used for gene therapy
XX CC purposes to treat diseases or disorders including cancer, immune-related
XX CC diseases, cardiovascular disease, brain or neuronal associated disease,
XX CC metabolic and inflammatory disorders. Accordingly, they exhibit
XX CC cytoprotective, neuroprotective, immunomodulator and antiinflammatory
XX CC activities. This polypeptide sequence is a human kinase protein sequence
XX CC of the invention.
XX
XX 60 Sequence 767 AA:
XX
XX Query Match 1 98.2%; Score 3670.5; DB 8; Length 787;
XX Best Local Similarity 91.6%; Pred. No. 2.8e-248;
XX Matches 721; Conservative 1; Mismatches 2; Indels 63; Gaps 2;
XX
XX QY 1 MSSAKRTLPPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNTYFLKTIG 60
XX DB 1 MSSAKRTLPPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNTYFLKTIG 60
XX
XX QY 61 KGNFAKYKLARHILITGKEVAVKIKDKTQLNSSSIQKLFREVRIMKVLNHPYIVLFEVIE 120
XX DB 61 KGNFAKYKLARHILITGKEVAVKIKDKTQLNSSSIQKLFREVRIMKVLNHPYIVLFEVIE 120
XX
XX QY 121 TEKTLVLYMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPTVHRDLRAEN 180
XX DB 121 TEKTLVLYMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPTVHRDLRAEN 180
XX
XX QY 121 TEKTLVLYMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPTVHRDLRAEN 180
XX DB 121 TEKTLVLYMEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKPTVHRDLRAEN 180
XX
XX QY 181 LLLDADNMVITKADFGSNEPTFGNKLDTFGGSPRYAAPLFGQKKYTGPEYDWSLGVIL 240
XX DB 181 LLLDADNMVITKADFGSNEPTFGNKLDTFGGSPRYAAPLFGQKKYTGPEYDWSLGVIL 240
XX
XX QY 181 LLLDADNMVITKADFGSNEPTFGNKLDTFGGSPRYAAPLFGQKKYTGPEYDWSLGVIL 240
XX DB 181 LLLDADNMVITKADFGSNEPTFGNKLDTFGGSPRYAAPLFGQKKYTGPEYDWSLGVIL 240
XX
XX QY 241 YTLVSGSLPFDGQULKELREVRVLRGKTRIPRYMSTDCENLLKKFLINPSSRGTLLEQIMK 300
XX DB 241 YTLVSGSLPFDGQULKELREVRVLRGKTRIPRYMSTDCENLLKKFLINPSSRGTLLEQIMK 300
XX
XX QY 301 DRMMNVGHEDEDELKPYVEPLPDYKDPRRTELMWSMGYTRERIDQSLVGQRVNEVMATYLL 360
XX DB 301 DRMMNVGHEDEDELKPYVEPLPDYKDPRRTELMWSMGYTRERIDQSLVGQRVNEVMATYLL 360

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QY 361 LGYKSELBDDTTTLKRPASADLTNSSAPSPSHKRVSVSANPKORRPSDQAGPAIPTSN 420
DB 361 LGYKSELBDDTTTLKRPASADLTNSSAPSPSHKRVSVSANPKORRPSDQAGPAIPTSN 420
QY 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPGLERKKTPTPTSTNSVLTSTN 480
DB 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPGLERKKTPTPTSTNSVLTSTN 480
QY 481 RSRNSPLLERASLIGQASIQNGKD----- 503
DB 481 RSRNSPLLERASLIGQASIQNGKDLTPGSRASTPASASAAVSAARPROHQKMGASVHPN 540
QY 504 -----STAPQRPVVASPSANHINSSGCGADPRNFRGVSSRSTFPAQ 546
DB 541 KASGLPPTESNCEVPSTAPQRPVVASPSAHNINSSGCGADPRNFRGVSSRSTFPAQ 600
QY 547 LRQVRDQONTPLYGTPASPGRHSQGRGASGSIFSKFTSKFV-----RRYLNRPES 597
DB 601 LRQVRDQONTPLYGTPASPGRHSQGRGASGSIFSKFTSKFVRNRLSPRARRLNRPES 660
QY 598 KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDAV 657
DB 661 KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDAV 720
QY 658 SCQSELHEKTMLCMGTPEHEDPVQWEMEVCTLPRLSLNGVPRKRLSGTSMARKNTASK 717
DB 721 SCQSELHEKTMLCMGTPEHEDPVQWEMEVCTLPRLSLNGVPRKRLSGTSMARKNTASK 780
QY 718 IANELKL 724
DB 781 IANELKL 787

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RESULT 9
ABR43965
ID ABR43965 standard; protein; 722 AA.

XX ABR43965;
XX AC ABR43965;
XX XX
XX DT 11-AUG-2003 (first entry)
XX DE Rat serine/threonine protein kinase MARK2.
XX KM Serine/threonine protein kinase; cytoprotective; antidiabetic; nootropic;
XX KM neuroprotective; antiinflammatory; analgesic; gene therapy; rat; MARK2;
XX KM chromosome 11q12-q13; enzyme.
XX OS Rattus norvegicus.
XX
XX PN WO2003033708-A2.
XX PD 24-APR-2003.
XX
XX PF 14-OCT-2002; 2002WO-EP011478.
XX PR 15-OCT-2001; 2001US-0328604P.
XX PR 27-FEB-2002; 2002US-0359688P.
XX PR 01-JUL-2002; 2002US-0392365P.
XX PA (FARB) BAYER AG.
XX PT Koehler RH;
XX PT WPI; 2003-403226/38.
XX DR
XX
XX PT New polynucleotide encoding a serine/threonine protein kinase
XX PT polypeptide, useful for preventing, ameliorating or treating diseases
XX PT associated with the protein kinase dysfunction, e.g. cancer, diabetes or
XX PT a CNS disorder.
XX PS Disclosure; Fig 1; 175bp; English.
XX

CC The invention relates to human serine/threonine protein kinase
 CC polypeptide and encoding polynucleotides. The polypeptides can be
 CC expressed by standard recombinant methodology. The polynucleotide and
 CC polypeptide are useful in preventing, ameliorating or treating diseases
 CC associated with serine/threonine protein kinase dysfunction. The diseases
 CC include cancer, diabetes, a CNS disorder or chronic obstructive pulmonary
 CC disease. These can also be used to treat pain associated with the above
 CC disorders. The protein kinase is also used in various diagnostic assays
 CC or in genetic testing. The present sequence represents a rat serine/
 CC threonine protein kinase MARK2
 CC
 XX Sequence 722 AA;

Query Match 97.8%; Score 3654; DB 6; Length 722;
 Best Local Similarity 97.8%; Pred. No. 3.5e-247;
 Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

QY 1 MSSARTPLPTINERTDEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 DB 1 MSSARTPLPTINERTDEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 QY 61 KGNFAKVKLARHILITGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHNPIYKLFVYIE 120
 DB 61 KGNFAKVKLARHILITGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHNPIYKLFVYIE 120
 QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIYHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIYHRDLKAEN 180
 QY 181 LLLDDNMNIKIADRGFSNEFTFGNKLDTFCGSPPYAAPLFOGKYDGPEVDVMSLGVIIL 240
 DB 181 LLLDDNMNIKIADRGFSNEFTFGNKLDTFCGSPPYAAPLFOGKYDGPEVDVMSLGVIIL 240
 QY 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPEYMSITDCENLLKFLINPSKRGTLBOIMK 300
 DB 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPEYMSITDCENLLKFLINPSKRGTLBOIMK 300
 QY 301 DRWNVGHGHEDELKPYVEPLPDYDOPRTEIMVSMGYTRREIODSLVGQRYNEVMATYLL 360
 DB 301 DRWNVGHGHEDELKPYVEPLPDYDOPRTEIMVSMGYTRREIODSLVGQRYNEVMATYLL 360
 QY 361 LGYSSSELEGGDTITLKRPSPADLTNSSAPSPSHVQSVSANPKORFSPQAGPAIPTS 420
 DB 361 LGYSSSELEGGDTITLKRPSPADLTNSSAPSPSHVQSVSANPKORFSPQAGPAIPTS 420
 QY 421 SYSKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTY 480
 DB 421 SYSKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTY 480
 QY 481 RSRNSPLLEPASLGOASTONGKOSTAPQRPVAPSAHNISSSGGAPDRTPRGVSSRS 540
 DB 481 RSRNSPLLEPASLGOASTONGKOSTAPQRPVAPSAHNISSSGGAPDRTPRGVSSRS 540
 QY 541 TFHAGQLROYDQONLTYGVTSPSPSGHSGRGASGSISPKTSTSFVRNINLEPSSKOR 600
 DB 541 TFHAGQLROYDQONLTYGVTSPSPSGHSGRGASGSISPKTSTSFVRNINLEPSSKOR 600
 QY 601 VETLRPHVVGSGGNDXKEEFREAKPRSLRFTWSMKTTSMEENEMREIRKVLANSQ 660
 DB 601 VETLRPHVVGSGGNDXKEEFREAKPRSLRFTWSMKTTSMEENEMREIRKVLANSQ 660
 QY 661 SELHEKMLLCMHGTGHEHDFVQWEMEVCKLPLSLINGVRFKRISGTSMAFKIASKIAN 720
 DB 661 SELHEKMLLCMHGTGHEHDFVQWEMEVCKLPLSLINGVRFKRISGTSMAFKIASKIAN 720
 QY 721 ELKFL 724
 DB 719 ELKFL 722

RESULT 10
 ADI30083
 ID ADI30083 standard; protein; 722 AA.

XX ADI30083;
 AC 22-Apr-2004 (first entry)
 DT Rat serine/threonine kinase protein.
 XX
 DE kinase; serine/threonine kinase; immune response; drug screening;
 KW tissue typing; pharmacogenomic analysis; tumour;
 KW brain anaplastic oligodendroglioma; lung carcinoma tissue;
 KW soft tissue leiomyosarcoma; gene therapy; transgenic animal; cytostatic;
 KW Rat; enzyme.
 XX
 OS Rattus norvegicus.
 NX US2003232408-A1.
 PN 18-DEC-2003.
 PD 21-OCT-2002; 2002US-00274194.
 PE 31-OCT-2001; 2001US-00984890.
 PR (APPL-) APPLERA CORP.
 PA Van C, Li Z, Neelam B, Difrancesco V, Beasley EM;
 PI WPI; 2004-061277/06.
 DR
 XX New peptides related to kinase protein subfamily useful for treating
 XX PT disorders associated with abnormal expression of kinase protein in
 XX PT testis, nervous tissue, fetal, lung, ovary tumor tissue.
 XX
 PS Disclosure; SEQ ID NO 4; 111pp; English.
 CC The invention relates to human kinase protein related to serine/threonine
 CC kinase subfamily and its corresponding nucleic acid sequence. The
 CC invention is useful to raise antibodies or to elicit immune response, as
 CC reagents in assays to determine the levels of protein in biological
 CC fluids, and as markers for tissues where the corresponding protein is
 CC expressed. It is also useful in drug screening assays, tissue typing and
 CC pharmacogenomic analysis. The sequences of the invention are useful in
 CC treating disorders associated with the absence of, inappropriate, or
 CC unwanted expression of kinase protein in testis, nervous tissue, foetal,
 CC lung, brain anaplastic oligodendroglioma, lung carcinoma tissue, soft
 CC tissue leiomyosarcoma, ovary tumor tissue, or germ cell tumour tissue.
 CC These are also useful in gene therapy and are useful as models for the
 CC development of human therapeutic targets, aid in the identification of
 CC therapeutic proteins and serve as targets for the development of human
 CC therapeutic agents that modulate protease activity in cells and tissues
 CC that express the kinase peptide. The host cells are useful in producing a
 CC kinase protein or peptide, and non-human transgenic animals. The present
 CC sequence is rat serine/threonine kinase protein.
 CC
 XX Sequence 722 AA;

Query Match 97.8%; Score 3654; DB 8; Length 722;
 Best Local Similarity 97.8%; Pred. No. 3.5e-247;
 Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

QY 1 MSSARTPLPTINERTDEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 DB 1 MSSARTPLPTINERTDEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKLTIG 60
 QY 61 KGNFAKVKLARHILITGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHNPIYKLFVYIE 120
 DB 61 KGNFAKVKLARHILITGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHNPIYKLFVYIE 120
 QY 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIYHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHQKFIYHRDLKAEN 180
 QY 181 LLLDDNMNIKIADRGFSNEFTFGNKLDTFCGSPPYAAPLFOGKYDGPEVDVMSLGVIIL 240

|||||
Db 181 LLLDADNMNLIKADPGFSNEFTFGKLDTPCGSPRYAAPELFOGKKYOGPEVDWMSLVIL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRVLRGKYRIPFYMTSTDCENLLKKFLILNPSKRGTLQIOMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRVLRGKYRIPFYMTSTDCENLLKKFLILNPSKRGTLQIOMK 300
Qy 301 DRMNNGHEDDELKPYVEPLPDYKDPRTTELWMSGTYREIIOQLVGOGRYNEVMATYLL 360
Db 301 DRMNNGHEDDELKPYVEPLPDYKDPRTTELWMSGTYREIIOQLVGOGRYNEVMATYLL 360
Qy 361 LGYKSSLEBDITTLKPRPSADLTNSSAPSPSHKVRQSVSANPKORRPSDQAPAIPTSN 420
Db 361 LGYKSSLEBDITTLKPRPSADLTNSSAPSPSHKVRQSVSANPKORRPSDQAPAIPTSN 420
Qy 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLTSTN 480
Db 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLTSTN 480
Qy 481 RSRNSPLLRASIGQASIONGKOSTAPORVPVAPSAHNISSSGAGDRTNPPRGVSSRS 540
Db 479 RSRNSPLLRASIGQASIONGKOSTAPORVPVAPSAHNISSSGAGDRTNPPRGVSSRS 538
Qy 541 TTFHAGQLRQVRDQNLPEYGTVPASPSGSHOGRRGASGISFSKFTSKFVRRLNLEPESKDR 600
Db 539 TTFHAGQLRQVRDQNLPEYGTVPASPSGSHOGRRGASGISFSKFTSKFVRRLNLEPESKDR 598
Qy 601 VETLRPHVVGSGGNDKEKEKEFEAKPRSLRPTWSMKTTSMEPNEMREIRKVLNANSCQ 660
Db 599 VETLRPHVVGSGGNDKEKEKEFEAKPRSLRPTWSMKTTSMEPNEMREIRKVLNANSCQ 658
Qy 661 SELHEKRMILCMGTPEGHEDPVQWEMEVCLPRLSLNGVYFKRISGTSMAFKNIASKIAN 720
Db 659 SELHEKRMILCMGTPEGHEDPVQWEMEVCLPRLSLNGVYFKRISGTSMAFKNIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 11
ADQ60238
ID ADQ60238 standard; protein; 722 AA.
XX
AC ADQ60238;
XX
DT 07-OCT-2004 (first entry)
XX
DE Rat serine/threonine kinase.
XX
KW allelic variant; orthologue; therapeutic; kinase activity modulation;
KW kinase associated disorder; rat; kinase;
KW serine/threonine kinase subfamily; enzyme.
XX
OS Rattus norvegicus.
XX
PN US2004137499-A1.
XX
PD 15-JUL-2004.
XX
PE 21-JAN-2004; 2004US-00760407.
XX
PR 31-OCT-2001; 2001US-00984890.
PR 21-OCT-2002; 2002US-00274194.
XX
PA (APPL-) APPLERA CORP.
XX
PI Yan C, Li Z, Neelam B, Diffrancesco V, Beasley EM,
XX
DR WPI, 2004-533359/51.
XX
PT New isolated human kinase peptide, useful for developing human
PT therapeutic targets, identifying therapeutic proteins, or as targets for

PT developing human therapeutic agents that modulate kinase activity in
XX cells and tissues.
XX
PS Disclosure, SEQ ID NO 4, 11pp, English.
XX
CC The invention describes an isolated peptide (1). The peptide comprises an
CC amino acid sequence selected from: an amino acid sequence comprising 724
CC of SEQ ID NO. 2, where the allelic variant is encoded by a nucleic acid
CC molecule that hybridizes to the opposite strand of a nucleic acid
CC molecule comprising 2175 bp (SEQ ID NO. 1) or 7595 bp (SEQ ID NO. 3); an
CC amino acid sequence of an orthologue of SEQ ID NO. 2, where the
CC orthologue is encoded by a nucleic acid molecule that hybridizes to the
CC opposite strand of SEQ ID NO. 1 or 3; or a fragment of SEQ ID NO. 2,
CC where the fragment comprises at least 10 contiguous amino acids. The
CC peptide sequence can be used as models for the development of human
CC therapeutic targets, aid in the identification of therapeutic proteins,
CC and serve as targets for the development of human therapeutic agents that
CC modulate kinase activity in cells and tissues and express the kinase.
CC They can also be used for biological assays related to kinases, in drug
CC screening assays in cell-based, or cell-free systems. It can also be used
CC to screen a compound for the ability to stimulate or inhibit interaction
CC between the kinase proteins and a molecule that normally interacts with
CC the kinase protein. They can also be used as targets for diagnosing a
CC disease or predisposition to disease mediated by the peptide, and for
CC treating disorders with an absence of, inappropriate, or unwanted
CC expression of the protein. This is the amino acid sequence of a rat
CC serine/threonine kinase used in a comparison with the human kinase of the
CC invention.
XX
SQ Sequence 722 AA;
Query Match 97.8%; Score 3654; DB 8; Length 722;
Best Local Similarity 97.8%; Pred. No. 3,5e-247;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
Qy 1 MSSARTPLPTLNERTDPTGHLGDSKPSKSMIRGNATGADQPHGNRLTKTG 60
Db 1 MSSARTPLPTLNERTDPTGHLGDSKPSKSMIRGNATGADQPHGNRLTKTG 60
Qy 61 KGNFAVKLARHILITGEVAVKIIDKTQNLSSSLQKLFRVRIIMKVLNHPNIYKLFEVIE 120
Db 61 KGNFAVKLARHILITGEVAVKIIDKTQNLSSSLQKLFRVRIIMKVLNHPNIYKLFEVIE 120
Qy 121 TEKTLVLYMEYASGGEVFDVLVHAGSMKEKAPAKTRQVSAVOYCHQKFTVHDLKAEN 180
Db 121 TEKTLVLYMEYASGGEVFDVLVHAGSMKEKAPAKTRQVSAVOYCHQKFTVHDLKAEN 180
Qy 181 LLLDADNMNLIKADPGFSNEFTFGKLDTPCGSPRYAAPELFOGKKYOGPEVDWMSLVIL 240
Db 181 LLLDADNMNLIKADPGFSNEFTFGKLDTPCGSPRYAAPELFOGKKYOGPEVDWMSLVIL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRVLRGKYRIPFYMTSTDCENLLKKFLILNPSKRGTLQIOMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRVLRGKYRIPFYMTSTDCENLLKKFLILNPSKRGTLQIOMK 300
Qy 301 DRMNNGHEDDELKPYVEPLPDYKDPRTTELWMSGTYREIIOQLVGOGRYNEVMATYLL 360
Db 301 DRMNNGHEDDELKPYVEPLPDYKDPRTTELWMSGTYREIIOQLVGOGRYNEVMATYLL 360
Qy 361 LGYKSSLEBDITTLKPRPSADLTNSSAPSPSHKVRQSVSANPKORRPSDQAPAIPTSN 420
Db 361 LGYKSSLEBDITTLKPRPSADLTNSSAPSPSHKVRQSVSANPKORRPSDQAPAIPTSN 420
Qy 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLTSTN 480
Db 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLTSTN 478
Qy 481 RSRNSPLLRASIGQASIONGKOSTAPORVPVAPSAHNISSSGAGDRTNPPRGVSSRS 540
Db 479 RSRNSPLLRASIGQASIONGKOSTAPORVPVAPSAHNISSSGAGDRTNPPRGVSSRS 538
Qy 541 TTFHAGQLRQVRDQNLPEYGTVPASPSGSHOGRRGASGISFSKFTSKFVRRLNLEPESKDR 600

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Db      539  TTHAGQLRQVRDQNLPGVTPASPSPGSHGQGRGASGSIFFSKFTISKFRRLNNEBESKOR 598
Qy      601  VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNDANSCQ 660
Db      599  VETLRPHVVGSGGDTKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNDANSCQ 658
Qy      661  SELHERMYMLCMHGTGPHGHEDPVQWMEVEYCKLPRLSLNGVRFKRLISGTSMAFNKIASKIAN 720
Db      659  SELHERMYMLCVHGTGPHGHEDPVQWMEVEYCKLPRLSLNGVRFKRLISGTSMAFNKIASKIAN 718
Qy      721  ELKL 724
Db      719  ELKL 722

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RESULT 12

AAR98227
ID AAR98227 standard; protein; 722 AA.

AC AAR98227;

DT 23-SEP-1996 (first entry)

DE Rat neuronal protein kinase MARK-2.

KW Neuronal protein kinase; NPK; microtubule associated protein; MAP;

KM tau protein; phosphorylation; NPK inhibitor; Alzheimer disease; cancer;

OS therapy; diagnosis.

XX Rattus norvegicus.

PN MO9613592-A2.

PD 09-MAY-1996.

PF 30-OCT-1995; 95WC-EP004258.

PR 28-OCT-1994; 94BP-00117122.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Mandelkow E, Mandelkow E, Biernat J, Drewes G;

DR WPI; 1996-251461/25.

XX DNA encoding neuronal protein kinase (NPK) - useful for identifying NPK

PT inhibitors for treatment of Alzheimer's disease and cancer.

XX Claim 1; Page 44-45; 77pp; English.

XX A novel rat neuronal protein kinase (AAR98227), designated NPK MARK-2, is

CC capable of phosphorylating a KXGS sequence motif in tau protein and

CC microtubule associated proteins MAP4, MAP2 and MAP2C (see also AAR98229-

CC 39 and AAW00850-54), causing their dissociation from microtubules.

CC Phosphorylation of human tau Ser-262 is indicative of the onset of

CC Alzheimer's disease. MARK-1 is the product of a cDNA clone obtd. from a

CC rat brain cDNA library by screening with probes derived from pig brain

CC peptide sequences (see also AAR98240-50). Another NPK, MARK-1 (AAR98226),

CC was similarly isolated. Inhibitors (e.g. antibodies) of NPKs are used to

CC treat Alzheimer's disease and cancer. NPKs are themselves used for in

CC vitro diagnosis and/or monitoring of Alzheimer's disease and cancer

XX Sequence 722 AA;

Query Match 97.5%; Score 3644; DB 2; Length 722;

Best Local Similarity 97.5%; Pred. No. 1.8e-246;

Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

Qy 1 MSGARTPLPLTNRDTEQPTLGHLSKPSKSNMIRGNSATSADQPHIGVRLIKTTIG 60

Db 1 MSGARTPLPLTNRDTEQPTLGHLSKPSKSNMIRGNSATSADQPHIGVRLIKTTIG 60

Qy 61 KGNFAKYKLARHILTGKEVAVKIIDKTOLNSSSLQKLFEVRIMKVLNHNPIVKLEFVIE 120

Db 61 KGNFAKYKLARHILTGKEVAVKIIDKTOLNSSSLQKLFEVRIMKVLNHNPIVKLEFVIE 120

Qy 121 TEKTLVYMEVYASGGVFPDVLVAHGRMKKEAAKROVAVANQYCHQKFIYHRDLKAEN 180

Db 121 TEKTLVYMEVYASGGVFPDVLVAHGRMKKEAAKROVAVANQYCHQKFIYHRDLKAEN 180

Qy 181 LLLDADNNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPLFOGKTYDGEVDVMSLGVL 240

Db 181 LLLDADNNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPLFOGKTYDGEVDVMSLGVL 240

Qy 241 YTLVSGSLPPDQNLKELBRVLRGKRIIPFYMSSTDCEMLKKFLILNPSKGTLEQIMK 300

Db 241 YTLVSGSLPPDQNLKELBRVLRGKRIIPFYMSSTDCEMLKKFLILNPSKGTLEQIMK 300

Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDRRTETLWVMSGYTEELIODSLVGRVNEWATYLL 360

Db 301 DRMMNVGHEDDELKPYVEPLPDYKDRRTETLWVMSGYTEELIODSLVGRVNEWATYLL 360

Qy 361 LGYKSELEBDITTLKPRPSADLTNSAPSPSHKYQSVSANPKORRPFSDQAPAIPTSN 420

Db 361 LGYKSELEBDITTLKPRPSADLTNSAPSPSHKYQSVSANPKORRPFSDQAPAIPTSN 420

Qy 421 SYSKTQSNMAENKPEEDRESGRKASTAKYPASPLQLERKKTTPPTNSVLTSTN 480

Db 421 SYSKTQSNMAENKPEEDRESGRKASTAKYPASPLQLERKKTTPPTNSVLTSTN 480

Qy 481 RSRNSPLLRASLIGQASLNGKDSAPORVPVAPSSAHNISSSGAPRTNPPRVSSRS 540

Db 481 RSRNSPLLRASLIGQASLNGKDSAPORVPVAPSSAHNISSSGAPRTNPPRVSSRS 540

Qy 541 TTHAGQLRQVRDQNLPGVTPASPSPGSHGQGRGASGSIFFSKFTISKFRRLNNEBESKOR 600

Db 541 TTHAGQLRQVRDQNLPGVTPASPSPGSHGQGRGASGSIFFSKFTISKFRRLNNEBESKOR 600

Qy 539 TTHAGQLRQVRDQNLPGVTPASPSPGSHGQGRGASGSIFFSKFTISKFRRLNNEBESKOR 598

Db 539 TTHAGQLRQVRDQNLPGVTPASPSPGSHGQGRGASGSIFFSKFTISKFRRLNNEBESKOR 598

Qy 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNDANSCQ 660

Db 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNDANSCQ 660

Qy 659 SELHERMYMLCMHGTGPHGHEDPVQWMEVEYCKLPRLSLNGVRFKRLISGTSMAFNKIASKIAN 720

Db 659 SELHERMYMLCMHGTGPHGHEDPVQWMEVEYCKLPRLSLNGVRFKRLISGTSMAFNKIASKIAN 720

Qy 721 ELKL 724

Db 719 ELKL 722

RESULT 13

ABU11830

ID ABU11830 standard; protein; 796 AA.

XX ABU11830;

DT 13-FEB-2003 (first entry)

DE Human MDDR polypeptide SEQ ID 777.

XX MDDR; human; disease detection and treatment molecule polypeptide;

XX anti-inflammatory; immunosuppressive; osteopathic; cytotoxic; anti-HIV;

XX haemostatic; nephrotoxic; antianemic; antiproliferative; hepatotropic;

XX gene therapy; protein replacement therapy; cell proliferative disorder;

XX cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;

XX anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;

XX Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;

XX psoriasis; hepatitis.

OS Homo sapiens.

PN WO200279449-A2.

PD 10-OCT-2002.

```

PF      27-MAR-2002; 2002MO-US009944.
XX
XX
PR      28-MAR-2001; 2001US-0279619P.
FR      29-MAR-2001; 2001US-0280067P.
PR      29-MAR-2001; 2001US-0280067P.
PR      29-MAR-2001; 2001US-0280068P.
PR      16-MAY-2001; 2001US-0291280P.
PR      17-MAY-2001; 2001US-0291829P.
PR      17-MAY-2001; 2001US-0291849P.
PR      19-JUN-2001; 2001US-0299428P.
PR      20-JUN-2001; 2001US-0299776P.
XX      20-JUN-2001; 2001US-0300001P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
PA
PI      Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI      DuFour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
PI      Daugherty SC, Dam TC, Liu TF, Nguyen AD, Kleefeld Y, Gerstein EH;
PI      Penvalle CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,
PI      Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX      WPI; 2003-058431/05.
DR      N-PDSB; ABX34820.
PT
PT      New purified disease detection and treatment molecule proteins and
PT      polypeptides, useful for diagnosing, treating or preventing cancers
PT      (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT      or hepatitis.
XX
XX      Claim 27; SEQ ID NO 777; 339pp + Sequence Listing; English.
XX
XX      This invention describes a novel disease detection and treatment molecule
XX      polypeptide (MDT) which has anti-inflammatory, immunosuppressive,
XX      osteopetrid, cytostatic, anti-HIV, haemostatic, nephrotropic,
XX      antianemid, antipsoriatic and hepatotropic activity. The polynucleotides
XX      and the polypeptides of the invention can be used for gene therapy,
XX      protein replacement therapy and are useful for treating a variety of
XX      diseases or conditions. These polypeptides or polynucleotides are
XX      particularly useful for diagnosing, treating or preventing cell
XX      proliferative disorders (e.g. cancers including adenocarcinoma,
XX      leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
XX      disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
XX      syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
XX      hepatitis. AbU11450-ABU11845 represent the MDT polynucleotides encoded
XX      by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
XX      The sequence data for this patent did not form part of the printed
XX      specification, but was obtained in electronic format from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 796 AA;
S0
Query Match          96.6%; Score 3610; DB 6; Length 796;
Best Local Similarity 92.4%; Pred No. 4.9e-244;
Matches 705; Conservative 3; Mismatches 1; Indels 54; Gaps 1
QY      16 TEQPTLGLHDKSPSSKSNMIRGRNSATSADDEPHIGNTRLLTKTGKNFAKYKLARIHLT 75
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DY      34 SSRPTGLHDKSPSSKSNMIRGRNSATSADDEPHIGNTRLLTKTGKNFAKYKLARIHLT 93
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      76 GKVAVAKIIDKTQLNSSLISLOKLFEVRRLMKLVNHENRYKLFEVITEKTLYLVMETASGG 135
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DY      94 GKVAVAKIIDKTQLNSSLISLOKLFEVRRLMKLVNHENRYKLFEVITEKTLYLVMETASGG 153
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      136 EVFDVLVAHGMRKEKARAKFROWSAVOYCHQKFIVRHDLKAENILLDADANNIKIADFG 195
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DY      154 EVFDVLVAHGMRKEKARAKFROIYSAVOYCHQKTIYHRDLKAENILLDADANNIKIADFG 213
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      196 FSNBEFTFGNKLDTCGSGPPYAAPBLFOGKKYDGPEVDWMSLGVIITLVSGSLPFDGNTL 255
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DY      214 FSNBEFTFGNKLDTCGSGPPYAAPBLFOGKKYDGPEVDWMSLGVIITLVSGSLPFDGNTL 273
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      256 KEIARRVLRGKRIFPYMWSTDCENILKKFLINPSKRGTLBOIMODRMNVGHEDDELKP 315
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db	274	HELDERVLRGKXRYLPFYMSDCEMLKKPFLIANDSKRGTLLEQIKMDRMMVGHEDDLK	333
Qy	316	YVEPLPDYKDBRRTELVMVSGYTFEEIQDSLVGQRYNEWATYLLGLYKSELEGGDTITL	375
Db	334	YVEPLPDYKDBRRTELVMVSGYTFEEIQDSLVGQRYNEWATYLLGLYKSELEGGDTITL	393
Qy	376	KPRPSADLTNSASPSGKHVQSRVSANPKORRFSDDGPAIPISNSYSKKTQSNNAENKR	435
Db	394	KPRPSADLTNSASPSGKHVQSRVSANPKORRFSDDGPAIPISNSYSKKTQSNNAENKR	453
Qy	436	PEEDRESGRKASSTAKYPASPLPELERRKTTPTPESTNSVLTSTNSRNSPLERASLQ	495
Db	454	PEEDRESGRKASSTAKYPASPLPELERRKTTPTPESTNSVLTSTNSRNSPLERASLQ	513
Qy	496	ASIONGKD-----	503
Db	514	ASIONGKDSLTPMGSRASSTASAAVAAAPRQHKQMSASVHPNKASGLPTESENCEVP	573
Qy	504	--STAPQRPVPASASANISSGGAAPRTYPPRRVSSRSSTPHAGQLAPVDQQLPYGYT	561
Db	574	RPSAPRPVPVPASASANISSGGAAPRTYPPRRVSSRSSTPHAGQLAPVDQQLPYGYT	633
Qy	562	PASPSGHSQGRGASGSIFSKFTSKFPRRLNIBESKDRVETTLRPHVVGSGANDKEEFP	621
Db	634	PASPSGHSQGRGASGSIFSKFTSKFPRRLNIBESKDRVETTLRPHVVGSGANDKEEFP	693
Qy	622	REAKPRSLRPTWSNKTTSMEPENMKREIRKVLVDANSQSELEHKYMLCMHGTPGHDF	681
Db	694	REAKPRSLRPTWSNKTTSMEPENMKREIRKVLVDANSQSELEHKYMLCMHGTPGHDF	753
Qy	682	VQWEMEVCKLPRLSLNGVPRFRISGTMAPRNITASKANLEKL	724
Db	754	VQWEMEVCKLPRLSLNGVPRFRISGTMAPRNITASKANLEKL	796
RESULT 14			
ADI40876			
ID	ADI40876	standard; protein; 799 AA.	
XX	AC	ADI40876;	
XX	DT	22-APR-2004 (first entry)	
XX	DE	Human kinase and phosphatase KPP-42 protein SEQ ID NO:42.	
KW	XX	human; kinase and phosphatase; KPP; enzyme; cardiovascular;	
KW	XX	antiartherosclerotic; hypotensive; vasotropic; antiinflammatory;	
KW	XX	antitumoral; anti-HIV; antiallergic; antiaesthetic; immunosuppressive;	
KW	XX	antihypertoid; dermatological; antidiabetic; nephrotropic; antigout;	
KW	XX	gastric/intestinal; neuroprotective; osteopathic; antiarthritic; uropathic;	
KW	XX	ophthalmological; antirheumatic; antiparkinsonian; nootropic;	
KW	XX	anticonvulsant; hepatotropic; CNS; antiparasitic; haemostatic;	
KW	XX	cytostatic; antileukemic; antiparasitic; antitubercular; antibacterial;	
KW	XX	virucide; protozoacide; fungicide; gene therapy; kinase modulator;	
KW	XX	phosphatase modulator; cardiovascular disease; immune system disorder;	
KW	XX	neurological disorder; growth and development disorder;	
KW	XX	cell proliferative disorder; infection.	
OS	XX	Homo sapiens.	
XX	XX	WO2004009778-A2.	
XX	XX	29-JAN-2004.	
XX	PD	18-JUL-2003; 2003WO-US022550.	
XX	PE	19-JUL-2002; 2002US-0397354P.	
XX	PR	02-AUG-2002; 2002US-0400509P.	
XX	PR	02-AUG-2002; 2002US-0400783P.	
XX	PR	15-AUG-2002; 2002US-0404027P.	
XX	XX	(INCY-) INCYTE CORP.	
XX	XX		

PI Hatella AJA, Emerling BM, Kable AE, Richardson TW, Becha SD,
PI Baugh MR, Tang YT, Jal PG, Lee SY, Griffin JA, Khare R,
PI Elliott VS, Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tiran UK,
PI Gunurajan R, Ding L, Margulis JP, Thornton MB, Forsythe LJ, Lee EA,
PI Gietzen KJ, Ramkumar J,
XX
XX WPI, 2004-132950/13.
DR N-PSDB, ADI40929.
XX
XX
PT New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.
XX
XX
PS Claim 1, SEQ ID NO 42; 330bp; English.
XX
XX
CC The present sequence represents a human kinase and phosphatase (KPP)
CC protein. KPP sequences have cardiovascular, antiarteriosclerotic,
CC hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV,
CC antiallergic, antidiabetic, immunosuppressive, antihypertoid,
CC dermatological, antidiabetic, nephrotropic, antigout, gastrointestinal,
CC neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological,
CC antineumatic, antiparkinsonian, nootropic, anticonvulsant, hepatocytic,
CC CNS, antipsoriatic, haemostatic, cytosolic, antilipemic, antiparasitic,
CC antihelminthic, antibacterial, virucide, protozoacide and fungicide
CC activities, and can be used in gene therapy, and as kinase modulators and
CC phosphatase modulators. KPP proteins, polynucleotides, agonists and
CC antagonists can be used for diagnosing, treating or preventing disorders
CC associated with aberrant expression of KPP, such as cardiovascular
CC diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris
CC or congestive heart failure), immune system disorders (e.g. AIDS,
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
CC gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis,
CC osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,
CC Sjogren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, dementia or
CC epilepsy), disorders affecting growth and development (e.g. cirrhosis,
CC hepatitis, mixed connective tissue disease, psoriasis or primary
CC thrombocytopenia), cell proliferative disorders (e.g.
CC hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. The KPP and
CC polynucleotides are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acids and kinases and
CC phosphatases, or for facilitating the drug discovery process, including
CC determination of efficacy, dosage, toxicity and pharmacology. The
CC polynucleotides encoding KPP are useful for creating transgenic animals
CC to model human disease.
XX
XX
SQ Sequence 799 AA;

Query Match 96.1%; Score 3589.5; DB 8; Length 799;
Best Local Similarity 88.7%; Pred. No.1.3e-242;
Matches 709; Conservative 4; Mismatches 11; Indels 75; Gaps 3;

QY 1 MSSARTPLPPLT-----NERDTEOPTGLHDSKPSKSMIRGRNS 40
DB 1 MEVAGSPFPFLOSVACILTLAHPAVGNILQHRRRGAGPTLGLHDSKPSKSMIRGRNS 60
QY 41 ATSADHOPHGNRLKTTGKGNFAVKLARHILTEKEVAVAVKIIDKTQUNSSSLQTLFPE 100
DB 61 ATSADHOPHGNRLKTTGKGNFAVKLARHILTEKEVAVAVKIIDKTQUNSSSLQTLFPE 120
QY 101 VRIIMKVLNPNIVKLEFEVITEKTLVLMVEYASGSEVPDYLVAHGMRKEKARAKPROV 160
DB 121 VRIIMKVLNPNIVKLEFEVITEKTLVLMVEYASGSEVPDYLVAHGMRKEKARAKPROV 180
QY 161 SAVOYCHQRYIYHRDIKAENLLADAMNLIKADFGSENEFTGKLTDFCGSPYAAPBL 220
DB 181 SAVOYCHQRYIYHRDIKAENLLADAMNLIKADFGSENEFTGKLTDFCGSPYAAPBL 240
QY 221 FQGGKYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELEERYLRGKRYRIPFMYSDCENL 280

DB 241 FQGGKYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELEERYLRGKRYRIPFMYSDCENL 300
QY 281 LKKFLLILNPSKGTLEQIKMDRMWVGHEDDLKPYVEPLPYKDPRTTELWVSGYTR 340
DB 301 LKKFLLILNPSKGTLEQIKMDRMWVGHEDDLKPYVEPLPYKDPRTTELWVSGYTR 360
QY 341 EIODSLVQGRVNEWATYLLILGYKSELEKGDITTLKPRSDLTNNSAPSPSHKYQSV 400
DB 361 EIODSLVQGRVNEWATYLLILGYKSELEKGDITTLKPRSDLTNNSAPSPSHKYQSV 420
QY 401 ANPKORFSDQ-AGPAIPTNSYSKKTOSNMENKRPEDDRSGKASTAVPASPPLPG 459
DB 421 ANPKORFSDQAGPAIPTNSYSKKTOSNMENKRPEDDRSGKASTAVPASPPLPG 480
QY 460 LERKKTTPPTSTNSVLTSTNSRNSPLLERASLQASIQNGK----- 503
DB 481 LERKKTTPPTSTNSVLTSTNSRNSPLLERASLQASIQNGKSLTMPGSRASVASA 540
QY 504 -----STAPQVPVAPSPAHN1SSSGG 525
DB 541 AVSAARPRQHKMSASVHPNKAAGLPTESNCEVPRPSTAPQVPVAPSPAHN1SSSGG 600
QY 526 ADPRTNFPRGVSRSSTFAGQLROYRDOONLPYGTVPASPSGSGRGAAGSIFSKPTS 585
DB 601 ADPRTNFPRGVSRSSTFAGQLROYRDOONLPYGTVPASPSGSGRGAAGSIFSKPTS 660
QY 586 KTVRRNLNPESSKDVETLRRPHVVGSGNDKEKEFRFAKPRSLRFTWSMKTSSMEPNE 645
DB 661 KTVRRNLNPESSKDVETLRRPHVVGSGNDKEKEFRFAKPRSLRFTWSMKTSSMEPNE 720
QY 646 MREIRKVLNDANSQSEIHEKYMILLCMGTGCHDFQVMEVYCLPRLSLNGVRFKIS 705
DB 721 MREIRKVLNDANSQSEIHEKYMILLCMGTGCHDFQVMEVYCLPRLSLNGVRFKIS 780
QY 706 GTSMAFKNIASKIANELKL 724
DB 781 GTSMAFKNIASKIANELKL 799

RESULT 15
AAE19050
ID AAE19050 standard; protein; 691 AA.
XX
XX
AC AAE19050;
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX Human PAR-1B alpha protein.
DE
XX
XX Human; Dishevelled associated kinase; PAR-1 kinase; enzyme; PAR-1A;
KW PAR-1B alpha; PAR-1B beta; PAR-1C; cancer; hyperproliferative disease;
KW antisense therapy; Dsh.
XX
XX Homo sapiens.
OS
XX
XX WO200210402-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 30-JUL-2001; 2001WO-US023981.
PF
XX
XX 28-JUL-2000; 2000US-0221860P.
PR
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Sun T, Feng J, Reinhard C, Fantl WJ, Williams LR,
PI
XX
XX WPI; 2002-206192/26.
DR
XX
XX N-PSDB; AAD30397.
XX
XX
PT Isolated nucleic acids encoding the human and Drosophila Dishevelled
PT associated kinase, referred to as PAR-1 kinase, useful for identifying
PT modulators which can be used for modulating, inhibiting or preventing the

PT growth of cancer cells.

XX
PS Claim 7; Page 283-284; 297pp; English.

CC The invention relates to Dishevelled (Dsh) associated kinase, referred to
CC as PAR-1 kinase in Drosophila and human homologues of PAR-1 referred to
CC as PAR-1a, PAR-1B (alpha and beta) and PAR-1c. The invention also
CC provides nucleic acid molecules encoding such proteins. PAR-1 activates
CC the Wnt pathway and is required for Wnt signaling in mammalian cells.
CC The PAR-1 modulators can be used to reduce the expression and/or
CC biological activity of PAR-1. They are useful for modulating, inhibiting
CC or preventing the growth of cancer cells. They are also useful for
CC treating other diseases of hyperproliferation. Sequences of the invention
CC are used in antisense therapy. The present sequence is human PAR-1B alpha
CC protein

XX
SQ Sequence 691 AA;

Query Match 95.4%; Score 3566; DB 5; Length 691;

Best Local Similarity 99.9%; Pred. No. 4.9e-241; Mismatches 0; Gaps 0;

Matches 690; Conservative 1; Indels 0; Indels 0; Gaps 0;

QY 34 MIRGRNSATSADQPHIGNYRLKTTIGKNFAKVKLARHILTGKEVAVKIIDKTQLNSSS 93
DB 1 MIRGRNSATSADQPHIGNYRLKTTIGKNFAKVKLARHILTGKEVAVKIIDKTQLNSSS 60
QY 94 LQKLFREVRIMKVLNHNPIYKLPVITEKTLILVMEYASGGEVFDYLVAHGRMKEKEAR 153
DB 61 LQKLFREVRIMKVLNHNPIYKLPVITEKTLILVMEYASGGEVFDYLVAHGRMKEKEAR 120
QY 154 AKFRQVSAVOYCHQKIVHRDLKAENLLDADNMTKIADFGFSNEPTFGNKLDTFCGSP 213
DB 121 AKFRQVSAVOYCHQKIVHRDLKAENLLDADNMTKIADFGFSNEPTFGNKLDTFCGSP 180
QY 214 PYAPBELFOGKXYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYM 273
DB 181 PYAPBELFOGKXYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYM 240
QY 274 SFDCEMLKKFLLINPSKRGTLLEQIMKORMNNGHEDDELKPYVEPLPDYKDPRTTELMV 333
DB 241 SFDCEMLKKFLLINPSKRGTLLEQIMKORMNNGHEDDELKPYVEPLPDYKDPRTTELMV 300
QY 334 SMGYTREBIQDSLVGORVNEVMATYLLGYKSSLEGGDTTLKPRPSADLTNSSAPSPSH 393
DB 301 SMGYTREBIQDSLVGORVNEVMATYLLGYKSSLEGGDTTLKPRPSADLTNSSAPSPSH 360
QY 394 KYGRSVSANPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEBEDRESGRKASTAKVP 453
DB 361 KYGRSVSANPKORRFSQAGPAIPTNSYSKKTQSNNAENKRPEBEDRESGRKASTAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLTSTNRSPNSPLERASTLGQASIQNGKDTAPQRYVPA 513
DB 421 ASPLPGLERKKTPTPTSTNSVLTSTNRSPNSPLERASTLGQASIQNGKDTAPQRYVPA 480
QY 514 SPBAHNISSSGGA PDRTPNPRGVSSRSTFHAQLROVRDOQNL PYGTPASPSPGHSQGR 573
DB 481 SPBAHNISSSGGA PDRTPNPRGVSSRSTFHAQLROVRDOQNL PYGTPASPSPGHSQGR 540
QY 574 GAGSIFSKFTSKFVRNLNLEPSKQVETLRPHVVGSGNDKEKEEFREAKPRSLRFTW 633
DB 541 GAGSIFSKFTSKFVRNLNLEPSKQVETLRPHVVGSGNDKEKEEFREAKPRSLRFTW 600
QY 634 SMKTTSSMEPNEMREIRKYLVDANSQSELEHEKYMILCMHGTPGHEDFVQWEMEVCCLPR 693
DB 601 SMKTTSSMEPNEMREIRKYLVDANSQSELEHEKYMILCMHGTPGHEDFVQWEMEVCCLPR 660
QY 694 LSLNGVRFKRIISGTSMAFKNIASKIANELKL 724
DB 661 LSLNGVRFKRIISGTSMAFKNIASKIANELKL 691

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:43:07 ; Search time 43 Seconds
(without alignments)
1256.882 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737

Sequence: 1 MSARTRPLTNRDTEQPT.....SGTSMAPKTIASKIANELKL 724

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodaca/1/1aa/5A COMB pep: *
2: /cgn2_6/ptodaca/1/1aa/5B COMB pep: *
3: /cgn2_6/ptodaca/1/1aa/6A COMB pep: *
4: /cgn2_6/ptodaca/1/1aa/6B COMB pep: *
5: /cgn2_6/ptodaca/1/1aa/PTUS COMB pep: *
6: /cgn2_6/ptodaca/1/1aa/backfile1 pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3737	100.0	724	4 US-09-984-890-2	Sequence 2, App1
2	3737	100.0	724	4 US-10-274-194-2	Sequence 2, App1
3	3654	97.8	722	4 US-09-984-890-4	Sequence 4, App1
4	3654	97.8	722	4 US-10-274-194-4	Sequence 4, App1
5	3644	97.5	722	4 US-08-817-8328-32	Sequence 32, App1
6	3566	95.4	691	4 US-09-949-016-8255	Sequence 8255, Ap
7	3566	95.4	691	4 US-09-949-016-8256	Sequence 8256, Ap
8	3515	94.1	745	4 US-09-523-849-36	Sequence 36, App1
9	2555	68.4	793	4 US-09-523-849-32	Sequence 32, App1
10	2513	67.2	692	4 US-09-949-016-7417	Sequence 7417, Ap
11	2513	67.2	692	4 US-09-949-016-7418	Sequence 7418, Ap
12	2464	65.9	729	4 US-08-817-8328-31	Sequence 31, App1
13	2399	64.2	729	2 US-08-677-298-2	Sequence 2, App1
14	2399	64.2	729	4 US-09-523-849-33	Sequence 33, App1
15	2394	64.2	724	4 US-09-949-016-8234	Sequence 8234, Ap
16	2381	63.7	713	4 US-09-538-092-1022	Sequence 1022, Ap
17	2381	63.7	713	4 US-09-949-016-6214	Sequence 6214, Ap
18	1130.5	30.3	764	4 US-09-523-849-35	Sequence 35, App1
19	1016	26.2	776	4 US-09-523-849-34	Sequence 34, App1
20	986	26.2	776	4 US-10-116-326-2	Sequence 2, App1
21	827	22.1	778	4 US-10-003-690-2	Sequence 2, App1
22	797.5	21.3	633	3 US-08-357-006C-43	Sequence 43, App1
23	797.5	21.3	633	3 US-09-538-092-212	Sequence 212, App
24	797.5	21.3	633	4 US-09-633-328B-3	Sequence 3, App1
25	797.5	21.3	633	4 US-09-824-735-3	Sequence 3, App1
26	793.5	21.2	668	4 US-09-930-181-2	Sequence 2, App1

28	757.5	20.3	512	4 US-09-633-328B-2	Sequence 2, App1
29	756.5	20.2	418	4 US-09-248-796A-1641	Sequence 1641, A
30	727.5	19.5	511	4 US-09-633-328B-4	Sequence 4, App1
31	711	19.0	703	4 US-10-116-326-6	Sequence 6, App1
32	710	19.0	557	4 US-09-949-016-10174	Sequence 10174, A
33	709	19.0	552	4 US-09-824-735-4	Sequence 4, App1
34	708	18.9	552	4 US-09-538-092-1212	Sequence 1212, Ap
35	705.5	18.9	552	3 US-08-557-006C-40	Sequence 40, App1
36	698	18.7	504	4 US-09-554-726A-10	Sequence 10, App1
37	694	18.6	257	2 US-07-857-224B-25	Sequence 25, App1
38	690.5	18.5	345	3 US-09-101-146-1	Sequence 1, App1
39	681	18.2	1064	4 US-09-538-092-154	Sequence 154, App
40	680	18.2	631	4 US-09-579-664B-11	Sequence 11, App1
41	680	18.2	631	4 US-10-355-975A-11	Sequence 11, App1
42	677	18.1	504	4 US-09-554-726A-14	Sequence 14, App1
43	675.5	18.1	630	4 US-10-355-975A-38	Sequence 38, App1
44	667	17.8	436	4 US-09-734-673-2	Sequence 2, App1
45	667	17.8	436	4 US-09-523-849-2	Sequence 2, App1

ALIGNMENTS

RESULT 1									
US-09-984-890-2									
; Sequence 2, Application US/09984890									
; Patent No. 6492156									
; GENERAL INFORMATION:									
; APPLICANT: YAN, Chunhua et al.									
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC									
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES									
; FILE REFERENCE: CL001306									
; CURRENT APPLICATION NUMBER: US/09/984, 890									
; CURRENT FILING DATE: 2001-10-31									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 724									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-984-890-2									
Query Match									
Best Local Similarity 100.0%; Score 3737; DB 4; Length 724;									
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MSARTRPLTNRDTEQPTLGHLDSPKSKSMWIRGNSATSGADEPHIGNRLKTTIG	60						
Db	1	MSARTRPLTNRDTEQPTLGHLDSPKSKSMWIRGNSATSGADEPHIGNRLKTTIG	60						
Qy	61	KGNFAVKLARHILLTGEKAVAKIIDTQUNSSLOQLFREVRIMKVLNHNIVKLFVIE	120						
Db	61	KGNFAVKLARHILLTGEKAVAKIIDTQUNSSLOQLFREVRIMKVLNHNIVKLFVIE	120						
Qy	121	TEKTLVLNVEYASGSEVFYLVAHGKMEKEAPAKRQVVSAYQYCHQKTYVHBDLKAEN	180						
Db	121	TEKTLVLNVEYASGSEVFYLVAHGKMEKEAPAKRQVVSAYQYCHQKTYVHBDLKAEN	180						
Qy	181	LILDDAMNLIKADFGSNEFTFGNKLDTFCGSPYAPALFOGKTYDGPVDVMSLGVL	240						
Db	181	LILDDAMNLIKADFGSNEFTFGNKLDTFCGSPYAPALFOGKTYDGPVDVMSLGVL	240						
Qy	241	YTLVSGSLPDDGQNLKELRERVLGKRYRIPFYVSTDCENLLKKFLILNPSKGTLEQIMK	300						
Db	241	YTLVSGSLPDDGQNLKELRERVLGKRYRIPFYVSTDCENLLKKFLILNPSKGTLEQIMK	300						
Qy	301	DRMANVGHEDDELKPYVEPLPDYKDRRRTELAMVSMGTREIIDSIVGQRYNEVMAITYLL	360						
Db	301	DRMANVGHEDDELKPYVEPLPDYKDRRRTELAMVSMGTREIIDSIVGQRYNEVMAITYLL	360						
Qy	361	LGYKSELEBDTTLTKPRPSADLTNSSAPSPSHKQVRSVANSKORRFSQQAIPATPSN	420						
Db	361	LGYKSELEBDTTLTKPRPSADLTNSSAPSPSHKQVRSVANSKORRFSQQAIPATPSN	420						

Db 361 LGYKSELEBDITTLKPRPSADITNSAPSPSHKQVSANPKORRFDQGPALPTSN 420
Qy 421 SYSKKTQSNNAENKREEDRESGRKASSTAKVPASPLPGLERKTTTPTSTNSVLTSTN 480
Db 421 SYSKKTQSNNAENKREEDRESGRKASSTAKVPASPLPGLERKTTTPTSTNSVLTSTN 480
Qy 481 RSRNSPLLRASLIGQASIONGKDSAPQRPVPAPEAHNISSSGAPDPTNPPRGVSSRS 540
Db 481 RSRNSPLLRASLIGQASIONGKDSAPQRPVPAPEAHNISSSGAPDPTNPPRGVSSRS 540
Qy 541 TFHAGQLROVDQOONLPYGVTPASPSGHSQGRGASGISFSTKFTSKFVRNLNBPESKDR 600
Db 541 TFHAGQLROVDQOONLPYGVTPASPSGHSQGRGASGISFSTKFTSKFVRNLNBPESKDR 600
Qy 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNANSCQ 660
Db 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNANSCQ 660
Qy 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAPKNIASKIAN 720
Db 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAPKNIASKIAN 720
Qy 721 ELKL 724
Db 721 ELKL 724

RESULT 2

US-10-274-194-2
/ Sequence 2, Application US/10274194
/ Patent No. 6706511
/ GENERAL INFORMATION:
/ APPLICANT: YAN, Chunhua et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ FILE REFERENCE: CL001306DIV
/ CURRENT APPLICATION NUMBER: US/10/274,194
/ CURRENT FILING DATE: 2003-12-18
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 724
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-274-194-2

Query Match 100.0%; Score 3737; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.3e-272;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSARTPLPTLNEDTBOPTLGHLDSPSSKSNMIRGRNSATSDADOPHIGNVRLKTTIG 60
Db 1 MSSARTPLPTLNEDTBOPTLGHLDSPSSKSNMIRGRNSATSDADOPHIGNVRLKTTIG 60
Qy 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNPNIVLFEVIE 120
Db 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNPNIVLFEVIE 120
Qy 121 TEKTLIYVMEYASGGEVFDYLVAHGRMKEKEARAKRQVVSAVOYCHQKFIVHRDLKAEN 180
Db 121 TEKTLIYVMEYASGGEVFDYLVAHGRMKEKEARAKRQVVSAVOYCHQKFIVHRDLKAEN 180
Qy 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKXYGPEVDWVSLGVTL 240
Db 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKXYGPEVDWVSLGVTL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLINPSKRGTLQIMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLINPSKRGTLQIMK 300
Qy 301 DWMNVGHEDDLKPYVEPLPDYKDPRTTELNVSMGYTTEETODSLVGQRINEVWATYLL 360
Db 301 DWMNVGHEDDLKPYVEPLPDYKDPRTTELNVSMGYTTEETODSLVGQRINEVWATYLL 360

Db 301 DWMNVGHEDDLKPYVEPLPDYKDPRTTELNVSMGYTTEETODSLVGQRINEVWATYLL 360
Qy 361 LGYKSELEBDITTLKPRPSADITNSAPSPSHKQVSANPKORRFDQGPALPTSN 420
Db 361 LGYKSELEBDITTLKPRPSADITNSAPSPSHKQVSANPKORRFDQGPALPTSN 420
Qy 421 SYSKKTQSNNAENKREEDRESGRKASSTAKVPASPLPGLERKTTTPTSTNSVLTSTN 480
Db 421 SYSKKTQSNNAENKREEDRESGRKASSTAKVPASPLPGLERKTTTPTSTNSVLTSTN 480
Qy 481 RSRNSPLLRASLIGQASIONGKDSAPQRPVPAPEAHNISSSGAPDPTNPPRGVSSRS 540
Db 481 RSRNSPLLRASLIGQASIONGKDSAPQRPVPAPEAHNISSSGAPDPTNPPRGVSSRS 540
Qy 541 TFHAGQLROVDQOONLPYGVTPASPSGHSQGRGASGISFSTKFTSKFVRNLNBPESKDR 600
Db 541 TFHAGQLROVDQOONLPYGVTPASPSGHSQGRGASGISFSTKFTSKFVRNLNBPESKDR 600
Qy 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNANSCQ 660
Db 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNMMEIRKVLNANSCQ 660
Qy 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAPKNIASKIAN 720
Db 661 SELHEKYMMLCMHGTGPHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAPKNIASKIAN 720
Qy 721 ELKL 724
Db 721 ELKL 724

RESULT 3

US-09-984-890-4
/ Sequence 4, Application US/09984890
/ Patent No. 6492156
/ GENERAL INFORMATION:
/ APPLICANT: YAN, Chunhua et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ FILE REFERENCE: CL001306
/ CURRENT APPLICATION NUMBER: US/09/984,890
/ CURRENT FILING DATE: 2001-10-31
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 722
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-984-890-4

Query Match 97.8%; Score 3654; DB 4; Length 722;
Best Local Similarity 97.8%; Pred. No. 8.9e-266;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MSSARTPLPTLNEDTBOPTLGHLDSPSSKSNMIRGRNSATSDADOPHIGNVRLKTTIG 60
Db 1 MSSARTPLPTLNEDTBOPTLGHLDSPSSKSNMIRGRNSATSDADOPHIGNVRLKTTIG 60
Qy 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNPNIVLFEVIE 120
Db 61 KGNFAKVLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNPNIVLFEVIE 120
Qy 121 TEKTLIYVMEYASGGEVFDYLVAHGRMKEKEARAKRQVVSAVOYCHQKFIVHRDLKAEN 180
Db 121 TEKTLIYVMEYASGGEVFDYLVAHGRMKEKEARAKRQVVSAVOYCHQKFIVHRDLKAEN 180
Qy 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKXYGPEVDWVSLGVTL 240
Db 181 LLLDADNMKIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFOGKXYGPEVDWVSLGVTL 240
Qy 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLINPSKRGTLQIMK 300
Db 241 YTLVSGSLPFDGQNLKELREVRILRGKYRIPTYMSTDCENILKKFLINPSKRGTLQIMK 300

Db 241 YTVVSGSLPFDGQNLKELRERVLRGKRYRIPFYMSTDCENLLKFFLLINPSKRGTLLEQIMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRRTLELMVSMGTREIIOQLVGOYNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRRTLELMVSMGTREIIOQLVGOYNEVMATYLL 360
Qy 361 LGYVSELEBDITTLKRPSPADLTNSSAPSPSHKVRQSVANPKORRFSQDAGPAITSN 420
Db 361 LGYVSELEBDITTLKRPSPADLTNSSAPSPSHKVRQSVANPKORRFSQDAGPAITSN 420
Qy 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSSTN 480
Db 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSSTN 480
Qy 481 RSRNSPLLEBASLQOASIQNGKOSTAPQRPVSPSAHNISSSGADPRTNPPRGVSSRS 540
Db 479 RSRNSPLLEBASLQOASIQNGKOSTAPQRPVSPSAHNISSSGADPRTNPPRGVSSRS 538
Qy 541 TFHAGOLROYRDOONLPYGVTPASPSGHSQGRGASGSIPTSKFTSKFVRRLNPEESKDR 600
Db 539 TFHAGOLROYRDOONLPYGVTPASPSGHSQGRGASGSIPTSKFTSKFVRRLNPEESKDR 598
Qy 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 660
Db 599 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 658
Qy 661 SELHEKTMILCMHGTPEHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Db 659 SELHEKTMILCMHGTPEHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 4
US-10-274-194-4
; Sequence 4, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C0001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-274-194-4

Query Match 97.8%; Score 3654; DB 4; Length 722;
Best Local Similarity 97.8%; Pred. No. 8.9e-266;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
Qy 1 MSARTEPLTINERDTEOPTLGHLDSPSSKSNMIRGRNSATSADDEPHIGNRLTKTG 60
Db 1 MSARTEPLTINERDTEOPTLGHLDSPSSKSNMIRGRNSATSADDEPHIGNRLTKTG 60
Qy 61 KGNPAKVKLARHILVTGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHNIVLFEVIE 120
Db 61 KGNPAKVKLARHILVTGKEVAVKIIDKTQLNSSSLQKLFREVRIMKVLNHNIVLFEVIE 120
Qy 121 TEKTLVYMEYASGGEVFDVLVAHGRMKEKARAKKFOVYSAVOYCHQKTIYHBDLKAEN 180
Db 121 TEKTLVYMEYASGGEVFDVLVAHGRMKEKARAKKFOVYSAVOYCHQKTIYHBDLKAEN 180
Qy 181 LLLDADNNIKIADPGFSEFTFGNKLDTPFGSGPPYAPLPEQKKYDGPEDVWMSLGVL 240
Db 181 LLLDADNNIKIADPGFSEFTFGNKLDTPFGSGPPYAPLPEQKKYDGPEDVWMSLGVL 240

Db 181 LLLDADNNIKIADPGFSEFTFGNKLDTPFGSGPPYAPLPEQKKYDGPEDVWMSLGVL 240
Qy 241 YTVVSGSLPFDGQNLKELRERVLRGKRYRIPFYMSTDCENLLKFFLLINPSKRGTLLEQIMK 300
Db 241 YTVVSGSLPFDGQNLKELRERVLRGKRYRIPFYMSTDCENLLKFFLLINPSKRGTLLEQIMK 300
Qy 301 DRMMNVGHEDDELKPYVEPLPDYKDPRRTLELMVSMGTREIIOQLVGOYNEVMATYLL 360
Db 301 DRMMNVGHEDDELKPYVEPLPDYKDPRRTLELMVSMGTREIIOQLVGOYNEVMATYLL 360
Qy 361 LGYVSELEBDITTLKRPSPADLTNSSAPSPSHKVRQSVANPKORRFSQDAGPAITSN 420
Db 361 LGYVSELEBDITTLKRPSPADLTNSSAPSPSHKVRQSVANPKORRFSQDAGPAITSN 420
Qy 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSSTN 480
Db 421 SYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTTPPTSTNSVLSSTN 480
Qy 481 RSRNSPLLEBASLQOASIQNGKOSTAPQRPVSPSAHNISSSGADPRTNPPRGVSSRS 540
Db 479 RSRNSPLLEBASLQOASIQNGKOSTAPQRPVSPSAHNISSSGADPRTNPPRGVSSRS 538
Qy 541 TFHAGOLROYRDOONLPYGVTPASPSGHSQGRGASGSIPTSKFTSKFVRRLNPEESKDR 600
Db 539 TFHAGOLROYRDOONLPYGVTPASPSGHSQGRGASGSIPTSKFTSKFVRRLNPEESKDR 598
Qy 601 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 660
Db 599 VETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLDA NSCQ 658
Qy 661 SELHEKTMILCMHGTPEHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 720
Db 659 SELHEKTMILCMHGTPEHEDFVQWEMEVCKLPRLSLNGVRPKRISGTSMAFKNIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722

RESULT 5
US-08-817-832B-32
; Sequence 32, Application US/08817832B
; Patent No. 6578691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6578691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-832B-32

Query Match 97.5%; Score 3644; DB 4; Length 722;
Best Local Similarity 97.5%; Pred. No. 5e-265;
Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

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QY 1 MSSARTPLPTLNRODTEOPLTGLHLDSPKSSKMMIGRNSATSDADOPHIGNRLKTTIG 60
DB 1 MSSARTPLPTLNRODTEOPLTGLHLDSPKSSKMMIGRNSATSDADOPHIGNRLKTTIG 60
QY 61 KGNFAKYLARHILITGKEVAVKIIDKTOLNSSLOKLFREVRIMKVLNHPNIYKLFVIE 120
DB 61 KGNFAKYLARHILITGKEVAVKIIDKTOLNSSLOKLFREVRIMKVLNHPNIYKLFVIE 120
QY 121 TEKTYLVMEYASGGEVFDYLVAHGRMKEKARQIVSAVOYCHHKETIYHRDLKAEN 180
DB 121 TEKTYLVMEYASGGEVFDYLVAHGRMKEKARQIVSAVOYCHHKETIYHRDLKAEN 180
QY 181 LILDDAMNLIKADPGSENEFTGKLDTPCGSPPYAPAPLFOGKTYDGPEDVWMSLGVL 240
DB 181 LILDDAMNLIKADPGSENEFTGKLDTPCGSPPYAPAPLFOGKTYDGPEDVWMSLGVL 240
QY 241 YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSDTCENLLKKFLILNPSKGTLEQIMK 300
DB 241 YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSDTCENLLKKFLILNPSKGTLEQIMK 300
QY 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELAVSMGYTREIIDSILVQRYNEVMAITYLL 360
DB 301 DRMMNVGHEDDELKPYVEPLPDYKDPRTTELAVSMGYTREIIDSILVQRYNEVMAITYLL 360
QY 361 LGKXSELESDTTLTKPRPADLTNSAPSPSHKQSVSANPKORRFSQAPALPTSN 420
DB 361 LGKXSELESDTTLTKPRPADLTNSAPSPSHKQSVSANPKORRFSQAPALPTSN 420
QY 421 SYBKTKQSNNAENKREBEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSSTN 480
DB 421 SYBKTKQSNNAENKREBEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSSTN 480
QY 481 RSNNSPLLEBASIGQASIONGKOSTAPORVPVAPSAHNISSSGAPDRTNPRGVSSRS 540
DB 481 RSNNSPLLEBASIGQASIONGKOSTAPORVPVAPSAHNISSSGAPDRTNPRGVSSRS 540
QY 541 TFHAGQLROVRDQNLPGVTPASPSGHSQGRGSGSIFSKTSGFVRNINLEPESKOR 600
DB 541 TFHAGQLROVRDQNLPGVTPASPSGHSQGRGSGSIFSKTSGFVRNINLEPESKOR 600
QY 601 VETLRPHVVGSGGNDKEKEFEAKPRSLRFTWSMKTTSSMEPNEMMRIRKVLANDNSCQ 660
DB 601 VETLRPHVVGSGGNDKEKEFEAKPRSLRFTWSMKTTSSMEPNEMMRIRKVLANDNSCQ 660
QY 661 SEIHEKYMILCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
DB 661 SEIHEKYMILCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
QY 721 ELKL 724
DB 719 ELKL 722
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RESULT 6
US-09-949-016-8255
Sequence 8255: Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8255
LENGTH: 691
TYPE: PRT
ORGANISM: Human
US-09-949-016-8255

Query Match 95.4%; Score 3566; DB 4; Length 691;
Best Local Similarity 99.9%; Pred. No. 3.4e-259;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 34 MIRGRNSATSADOPHIGNRYRLKTIKGKGFAYKLARHILITGKEVAVKIIDKTOLNSS 93
DB 1 MIRGRNSATSADOPHIGNRYRLKTIKGKGFAYKLARHILITGKEVAVKIIDKTOLNSS 60
QY 94 LOKLFREVRIMKVLNHPNIVKLFVYIETETKTYLVMEYASGGEVFDYLVAHGRMKEKAR 153
DB 61 LOKLFREVRIMKVLNHPNIVKLFVYIETETKTYLVMEYASGGEVFDYLVAHGRMKEKAR 120
QY 154 AKFROVYSAVOYCHOKETIYHRDLKAENLILDDAMNLIKADPGSENEFTGKLDTPCGSP 213
DB 121 AKFROVYSAVOYCHOKETIYHRDLKAENLILDDAMNLIKADPGSENEFTGKLDTPCGSP 180
QY 214 PYAAPBLFOGKTYDGPEDVWMSLGVLITLVSGSLPFDGQNLKELRERVLRGKYRIPFY 273
DB 181 PYAAPBLFOGKTYDGPEDVWMSLGVLITLVSGSLPFDGQNLKELRERVLRGKYRIPFY 240
QY 274 STDCENLKKFLILNPSKGTLEQIMKORMMNVGHEDDELKPYVEPLPDYKDPRTTELAV 333
DB 241 STDCENLKKFLILNPSKGTLEQIMKORMMNVGHEDDELKPYVEPLPDYKDPRTTELAV 300
QY 334 SMGYTREIIDSILVQRYNEVMAITYLLGYKXSELESDTTLTKPRPADLTNSAPSPSH 393
DB 301 SMGYTREIIDSILVQRYNEVMAITYLLGYKXSELESDTTLTKPRPADLTNSAPSPSH 360
QY 394 KYORSVSNPKORRFSQAPALPTSNBSYKKTQSNNAENKREBEDRESGRKASTAKVP 453
DB 361 KYORSVSNPKORRFSQAPALPTSNBSYKKTQSNNAENKREBEDRESGRKASTAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLSSTNSRNSPLLEBASIGQASIONGKOSTAPORVPA 513
DB 421 ASPLPGLERKKTPTPTSTNSVLSSTNSRNSPLLEBASIGQASIONGKOSTAPORVPA 480
QY 514 SPSAHNISSSGAPDRTNPRGVSSRSTFHAGQLROVRDQNLPGVTPASPSGHSQGR 573
DB 481 SPSAHNISSSGAPDRTNPRGVSSRSTFHAGQLROVRDQNLPGVTPASPSGHSQGR 540
QY 574 GASGSI FSKTSGFVRNINLEPESKORVETLRPHVVGSGGNDKEKEFEAKPRSLRFTW 633
DB 541 GASGSI FSKTSGFVRNINLEPESKORVETLRPHVVGSGGNDKEKEFEAKPRSLRFTW 600
QY 634 SMKTTSSMEPNEMMRIRKVLANDNSCOSIHEKYMILCMHGTPGHEDFVQWEMEVCKLP 693
DB 601 SMKTTSSMEPNEMMRIRKVLANDNSCOSIHEKYMILCMHGTPGHEDFVQWEMEVCKLP 660
QY 694 ISLNGVRFKRIISGTSMAFKNIASKIANELKL 724
DB 661 ISLNGVRFKRIISGTSMAFKNIASKIANELKL 691
```

RESULT 7
US-09-949-016-8256
Sequence 8256: Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 8256
: LENGTH: 691
: TYPE: PR1
: ORGANISM: Human
US-09-949-016-8256

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```

Query Match      95.4%; Score 3566; DB 4; Length 691,
Best Local Similarity 99.9%; Pred. No. 3,4e-259;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 34 MINGRNSATSADBOPIHIGNRRLKTIKGNFAVKYKLARHILITGEVAVKIIDKTQNLSSS 93
DB 1 MINGRNSATSADBOPIHIGNRRLKTIKGNFAVKYKLARHILITGEVAVKIIDKTQNLSSS 60
QY 94 LQKLFREVRIMKVLNHNIVKLFVETETKTYLMEVYASGGEVFDVLVHGRMKEAR 153
DB 61 LQKLFREVRIMKVLNHNIVKLFVETETKTYLMEVYASGGEVFDVLVHGRMKEAR 120
QY 154 AKPROVSAVOYCHOKEIVHRDLKAENLLDADNMIKIDFGFSNEFTFGNKIDTFGCGSP 213
DB 121 AKPROVSAVOYCHOKEIVHRDLKAENLLDADNMIKIDFGFSNEFTFGNKIDTFGCGSP 180
QY 214 PYAAPBELFOGKKYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIIPFM 273
DB 181 PYAAPBELFOGKKYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIIPFM 240
QY 274 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELMV 333
DB 241 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELMV 300
QY 334 SMGYTREIODSLVGOQRYNEVMATYLLGYKSELEGGDTITLKRPSADLTNSGAPSPSH 393
DB 301 SMGYTREIODSLVGOQRYNEVMATYLLGYKSELEGGDTITLKRPSADLTNSGAPSPSH 360
QY 394 KVOQSVSANPKORRFSDOAGPAIPTNSYSKKTQSNNAENKRPEDESEGRKASTAKVP 453
DB 361 KVOQSVSANPKORRFSDOAGPAIPTNSYSKKTQSNNAENKRPEDESEGRKASTAKVP 420
QY 454 ASPLPGLERKKTTPPTSTNSVLSTSTNRKSNPLERASIGQASIQNGKOSTAPQRPVA 513
DB 421 ASPLPGLERKKTTPPTSTNSVLSTSTNRKSNPLERASIGQASIQNGKOSTAPQRPVA 480
QY 514 SPASAHNISSGGAPDRNPPRGVSSRSTFHAQOLROVRDOONLPYGVTPASPSSGSGGR 573
DB 481 SPASAHNISSGGAPDRNPPRGVSSRSTFHAQOLROVRDOONLPYGVTPASPSSGSGGR 540
QY 574 GASGSIFSFKTSKVRRLNEPESKDRVETLRRPHVVGSGNDKEKEEFREAKRPSRLFTW 633
DB 541 GASGSIFSFKTSKVRRLNEPESKDRVETLRRPHVVGSGNDKEKEEFREAKRPSRLFTW 600
QY 634 SMKTTSMENEMNEMREIRKYLVDANSQSELEHEKMYLLCHGTRGHEHFPVOMENEVCKLPR 693
DB 601 SMKTTSMENEMNEMREIRKYLVDANSQSELEHEKMYLLCHGTRGHEHFPVOMENEVCKLPR 660
QY 694 LSLINGVFRKISGTSMAFKNIASIKIANELK 724
DB 661 LSLINGVFRKISGTSMAFKNIASIKIANELK 691

```

RESULT 8
US-09-523-849-36

```

: Sequence 36, Application US/09523849
: Patent No. 6458561
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Molteni, Angela
: APPLICANT: Magnaghi, Paola
: APPLICANT: Bosotti, Roberta
: APPLICANT: Scaccheri, Emanuela
: APPLICANT: Isacchi, Antonella
: APPLICANT: Hodgson, Dave
: TITLE OF INVENTION: HUMAN NIM1 KINASE
: FILE REFERENCE: PC-0009 US
: CURRENT APPLICATION NUMBER: US/09/523,849
: CURRENT FILING DATE: 2000-03-13
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PERL Program
: SEQ ID NO 36
: LENGTH: 745
: TYPE: PR1
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Genbank Accession No. 6458561 91749794
US-09-523-849-36

```

```

Query Match      94.1%; Score 3515; DB 4; Length 745;
Best Local Similarity 92.3%; Pred. No. 2,5e-255;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

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QY 34 MINGRNSATSADBOPIHIGNRRLKTIKGNFAVKYKLARHILITGEVAVKIIDKTQNLSSS 93
DB 1 MINGRNSATSADBOPIHIGNRRLKTIKGNFAVKYKLARHILITGEVAVKIIDKTQNLSSS 60
QY 94 LQKLFREVRIMKVLNHNIVKLFVETETKTYLMEVYASGGEVFDVLVHGRMKEAR 153
DB 61 LQKLFREVRIMKVLNHNIVKLFVETETKTYLMEVYASGGEVFDVLVHGRMKEAR 120
QY 154 AKPROVSAVOYCHOKEIVHRDLKAENLLDADNMIKIDFGFSNEFTFGNKIDTFGCGSP 213
DB 121 AKPROVSAVOYCHOKEIVHRDLKAENLLDADNMIKIDFGFSNEFTFGNKIDTFGCGSP 180
QY 214 PYAAPBELFOGKKYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIIPFM 273
DB 181 PYAAPBELFOGKKYDGEVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIIPFM 240
QY 274 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELMV 333
DB 241 STDCENLLKKFLLINPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELMV 300
QY 334 SMGYTREIODSLVGOQRYNEVMATYLLGYKSELEGGDTITLKRPSADLTNSGAPSPSH 393
DB 301 SMGYTREIODSLVGOQRYNEVMATYLLGYKSELEGGDTITLKRPSADLTNSGAPSPSH 360
QY 394 KVOQSVSANPKORRFSDOAGPAIPTNSYSKKTQSNNAENKRPEDESEGRKASTAKVP 453
DB 361 KVOQSVSANPKORRFSDOAGPAIPTNSYSKKTQSNNAENKRPEDESEGRKASTAKVP 420
QY 454 ASPLPGLERKKTTPPTSTNSVLSTSTNRKSNPLERASIGQASIQNGKOSTAPQRPVA 513
DB 421 ASPLPGLERKKTTPPTSTNSVLSTSTNRKSNPLERASIGQASIQNGKOSTAPQRPVA 480
QY 514 SPASAHNISSGGAPDRNPPRGVSSRSTFHAQOLROVRDOONLPYGVTPASPSSGSGGR 573
DB 481 SPASAHNISSGGAPDRNPPRGVSSRSTFHAQOLROVRDOONLPYGVTPASPSSGSGGR 540
QY 574 GASGSIFSFKTSKVRRLNEPESKDRVETLRRPHVVGSGNDKEKEEFREAKRPSRLFTW 633
DB 541 GASGSIFSFKTSKVRRLNEPESKDRVETLRRPHVVGSGNDKEKEEFREAKRPSRLFTW 600
QY 634 SMKTTSMENEMNEMREIRKYLVDANSQSELEHEKMYLLCHGTRGHEHFPVOMENEVCKLPR 693
DB 601 SMKTTSMENEMNEMREIRKYLVDANSQSELEHEKMYLLCHGTRGHEHFPVOMENEVCKLPR 660

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Qy	640	SMENPMEMRIRKYLANS	QOSLHEKTMLLQHGTPGHEDPVOEMEWCKLPRLSLNGV	699
Db	661	SMENPMEMRIRKYLANS	QOSLHEKTMLLQHGTPGHEDPVOEMEWCKLPRLSLNGV	720
Qy	700	RFKRISGTSMAFKNIASKIANEKL	724	
Db	721	RFKRISGTSMAFKNIASKIANEKL	745	
RESULT 9				
US-09-523-849-32				
/ Sequence 32, Application US/09523849				
/ Patent No. 6458561				
/ GENERAL INFORMATION:				
/ APPLICANT: Bandman, Olga				
/ APPLICANT: Molteni, Angela				
/ APPLICANT: Magnaghi, Paola				
/ APPLICANT: Bobotli, Roberta				
/ APPLICANT: Scacheri, Emanuela				
/ APPLICANT: Isaacchi, Antonella				
/ APPLICANT: Hodgson, Dave				
/ TITLE OF INVENTION: HUMAN NIM1 KINASE				
/ FILE REFERENCE: PC-0009 US				
/ CURRENT APPLICATION NUMBER: US/09/523,849				
/ NUMBER OF SEQ ID NOS: 39				
/ SOFTWARE: PERL Program				
/ SEQ ID NO 32				
/ LENGTH: 793				
/ TYPE: PRT				
/ ORGANISM: Rattus norvegicus				
/ FEATURE:				
/ NAME/KEY: misc feature				
/ OTHER INFORMATION: GenBank Accession No. 6458561 g2052189				
US-09-523-849-32				
Query Match 68.4%; Score 2555; DB 4; Length 793;				
Best Local Similarity 65.5%; Pred. No. 3,1e-183;				
Matches 525; Conservative 82; Mismatches 105; Indels 90; Gaps 14				
Qy	3	SARPTLPPTNEDTQOPTL--GHLD-----SKPSSKSMIRGRNATGA-DEPHIGNYR	54	
Db	2	SARPTLPPTNEDTNTHTSVSDYTETHIPTTSSSRQNIPIGRNITATBOEPHIGNYR	61	
Qy	55	LLKTTIGKGNFAKYKLARHLITGEKVAVKIIDTQLNSSLQTLFREVIMKVLNPNIVK	114	
Db	62	LQTTIGKGNFAKYKLARHLITGREVAVKIIDTQLNPNISLQTLFREVIMKVLNPNIVK	121	
Qy	115	LFEVLETKTLYLVNVEYASGGVEFYLVAHGMRKEKARAFROYVASVOYCHOKFIYHR	174	
Db	122	LFEVLETKTLYLVNVEYASGGVEFYLVAHGMRKEKARAFROYVASVOYCHOKFIYHR	181	
Qy	175	DLKAENLLDDADMNKIKIDPFGSNEFTGKNLIDTCGSPPYAAPLFGKKYDGEVDVW	234	
Db	182	DLKAENLLDDADMNKIKIDPFGSNEFTYGNLIDTCGSPPYAAPLFGKKYDGEVDVW	241	
Qy	235	SLGVLLYTLVSGSLPFDQONLKELEERYLRGKRIIPFTMSIDCENLLKKFLILNPSKRG	294	
Db	242	SLGVLLYTLVSGSLPFDQONLKELEERYLRGKRVFPFTMSIDCENLLKKFLILNPSKRG	301	
Qy	295	LEQIMKDRMNVVGHEDDEKPYVEPLPYXQPRRELMVSVGGYREELQDSVGNORVNEV	354	
Db	302	LEQIMKDRMNVVGHEDDEKPYVEPLPYXQPRRELMVSVGGYREELQDSVGNORVNEV	361	
Qy	355	MATYILLGKSSSELEG-----DTTLKRPSPADLTNNSAPSPSH-KVQSVSANPKQRR	407	
Db	362	MATYILLGKRPPEFGESLESGNLCQSRSPSSDNLNNTLQSPHLKQVRSISANQQR	421	
Qy	408	FSDAGAPLIPNSNGSKTOSNMNAENKRPED-DESGKASST-----AKYPAPPLGLE	461	
Db	422	FSDAGAPLIPPAVYITKRPQANVSESQKEKEMWDQYARLIGSTTVGSKSEVTASPLVGP	481	
Qy	462	RKKTPTPTSTNVLSTSTNRSRNPPLERASIDQASIONGKDS-----	504	

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Db          482 RKKSAGPS-NNYYSGSMRTMTTYVCERSTDRPAAALQNRDSSLITEMSASMSTGTV    540
              ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy          505 -----TAP-----ORVPVSPSAHNISSGGA    526
Db          541 ASAGPSARPHOKSMSTSGHPKIVTLPTIKDGSEAVRPGTAORVPVAPSAHSISAS--T    598
Qy          527 PDRTNPPRGVSRSRTFACQLRQVRPOOQLPYGVTPASP-----GHOGGRGAGSGIFSK    582
Db          599 PDRTRPRFGSSSSTHGEOI---RRSRSAAYGGPRASPSPHDPAALAHAARGSTGLISK    655
Qy          583 FTSKYPRNLNEPESKDREVETLPPHVVGSGNDKEEFPREAVPRSLRFTWSMKTTSME    642
Db          656 ITSEFVRADPREEBAGARDTDYAR----GSSEGEPKDKEEGEAKPRSLRFTWSMKTTSMD    711
Qy          643 PNEMMEIRVLVDANSQSSELEHKMYLLCMHGTFPGHEDPFOMTEAVCKLPRLSLNGVRFK    702
Db          712 PDMVAEIRKVLVDANTCDVEQRERFLPLFCVHGDAODSLVOMEAVECKLPRLSLNGVRFK    771
Qy          703 RISGTSMAREKNIAASKIANELKT    724
Db          772 RISGTSIAREKNIAASKIANELKL    793

RESULT 10
US-09-949-016-7417
; Sequence 7417, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7417
; LENGTH: 602
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-7417

Query Match      67.2%; Score 2513; DB 4; Length 602;
Best Local Similarity 88.1%; Pred. No. 36-180;
Matches 504; Conservative 5; Mismatches 19; Indels 44; Gaps 5;

Qy          16 TEQPTLGHLDSPSSKSNMIRGNATSADBOPIGNTRLTKTGKNFAKYKLARIHIIT    75
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db          34 SSRPTLGHLDSPSSKSNMIRGNATSADBOPIGNTRLTKTGKNFAKYKLARIHIIT    93
Qy          76 GEVNAVKKIIDKTOLNSSSLQKLFREVRIMKYLNNHNYIKLFVITEBKTLTYLWMEYASGG    135
Db          94 GKNAVVKIIIDKTOLNSSSLQKLFREVRIMKYLNNHNYIKLFVITEBKTLTYLWMEYASGG    153
Qy          136 EVFDYLVAHGEMKEEKARAFROVVSAVOYCHQKFIVARDIKAENILLDADANNIKIADFG    195
Db          154 EVFDYLVAHGEMKEEKARAFROIYSAVOYCHQKFIVARDIKAENILLDADANNIKIADFG    213
Qy          196 FSNNETFENKLDTPCGSPFYAAPELFOGKXYDGPVNDVWSLGVIILITYVSGSLPFDDGNLT    255
Db          214 FSNNETFENKLDTPCGSPFYAAPELFOGKXYDGPVNDVWSLGVIILITYVSGSLPFDDGNLT    273
Qy          256 KELEBRVLGKCYRPFWYSTDCENLLKKFELLINFSKRGTLEQIMKDRMMNVGHEDDELKP    315
Db          274 KELEBRVLGKCYRPFWYSTDCENLLKKFELLINFSKRGTLEQIMKDRMMNVGHEDDELKP    333

```


Qy	316	YVEELPYKDPRTTELMVSNMGYTRREIQQSLVGQRYNEVMATYLLLGKXSELEGDTTTL	375
Db	334	YVEELPYKDPRTTELMVSNMGYTRREIQSLVGQRYNEVMATYLLLGKXSELEGDTTTL	393
Qy	376	KPRPSADLTNLSAPSPSHKYQSVSANKPRFRPSDAQPAIPTNSYSKKTQSNNAENKR	435
Db	394	KPRPSADLTNLSAPSPSHKYQSVSANKPRFRPSDAQPAIPTNSYSKKTQSNNAENKR	453
Qy	436	PEEDRESGRVASTATAVPASPPLGGERKKTTPETPTNSVLTSTNTRSNNSPLTERASTGQ	495
Db	454	PEEDRESGRVASTATAVPASPPLGGERKKTTPETPTNSVLTSTNTRSNNSPLTERASTGQ	513
Qy	496	ASLQNGKDS-TAB-QEVPVASPBA-----HNISSGCAPDRTN--FP	533
Db	514	ASLQNGKDSLTIMGSRASTASTASAAVAARPRQHOKMSMASVHPKASGLPPTESNCEVP	573
Qy	534	RGVSRSTFPAAGQLRQVRDQQLPYVTTPASP	565
Db	574	R-----PROVPACP	583

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11 RESULT 11
US-09-949-016-7418
Sequence 7418, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7418
LENGTH: 602
TYPE: PRT
ORGANISM: Human
US-09-949-016-7418

```

Query Match	67.2%	Score 2513	DB 4	Length 602
Best Local Similarity	88.1%	Pred. No. 3e-180		
Matches	504	Conservative	5	Mismatches 19
			Indels 44	Gaps 5
QY	16	TEQPTLGHLDSPSSKSNMIRGNSATSAD	EQPHIGNRYLLKTTIGKPNFAKYLARHLLT	75
	:	:	:	:
Db	34	SSRPFTLGHLDSPSSKSNMIRGNSATSAD	EQPHIGNRYLLKTTIGKPNFAKYLARHLLT	93
QY	76	GKEVAVVKIIDTQOLNSSLSLOKLPREVR	IMKTLNHNLYKLEVEVIEETKTLYLWNEYASGG	135
Db	94	GKEVAVVKIIDTQOLNSSLSLOKLPREVR	IMKTLNHNLYKLEVEVIEETKTLYLWNEYASGG	153
QY	136	EVFPDYLVAHGEMKEKEAKAFROYVSAV	OYCHOKIYVRDLKAENLLDADAMNKIADFG	195
Db	154	EVFPDYLVAHGEMKEKEAKAFROYVSAV	OYCHOKIYVRDLKAENLLDADAMNKIADFG	213
QY	196	FSNEFTFGNKLDTECGSPBPYAPAPEL	FOGKATYDGEVDVWSLGVLLYTLVSGSLPFDGQNL	255
Db	214	FSNEFTFGNKLDTECGSPBPYAPAPEL	FOGKATYDGEVDVWSLGVLLYTLVSGSLPFDGQNL	273
QY	256	KELEBRVLRGKRYRIPFYWSTDCENLLK	FFLLNPSKRGTELOIMKDRMANYGHEDDELXP	315
Db	274	KELEBRVLRGKRYRIPFYWSTDCENLLK	FFLLNPSKRGTELOIMKDRMANYGHEDDELXP	333
QY	316	YVEBLPQYKDDRRRLTELWWSMGVYTB	EEOISLVGQRYNVMAVTAUULLYLGKXSELGDDTTL	375
Db	334	YVEBLPQYKDDRRRLTELWWSMGVYTB	EEOISLVGQRYNVMAVTAUULLYLGKXSELGDDTTL	393

Qy	376	KPPPSADLTNNSAPSPSHVQKQSVANPQRKRFSPQAPALPTNSVSKTQSNNAENKR	435
Db	394	KPPPSADLTNNSAPSPSHVQKQSVANPQRKRFSPQAPALPTNSVSKTQSNNAENKR	455
Qy	436	PEEDRESGKASSTAKVPASPLGLERKKTPTPTSTSVLSTSTNRSNPLERASLGQ	495
Db	454	PEEDRESGKASSTAKVPASPLGLERKKTPTPTSTSVLSTSTNRSNPLERASLGQ	513
Qy	496	ASIQNKDS-TAP-QRVVAPSPA-----NHSSGCAPDNT--FP	533
Db	514	ASIQNKDSILTMGSRASSTASAAVSAARPROHOKSNASVHPNKASGLPTESNCEVP	573
Qy	534	RGVSRSTFHAQGLRVDQQLPYGLVPASP	565
Db	574	R-----PQVPRPACP	583

RESULT 12 832B-31
 ; Sequence 31, Application US/08817832B
 ; Patent No. 6579691
 ; General Information:
 ; APPLICANT: MANDELKOW, Eckhard, et al.
 ; TITLE OF INVENTION: No. 6579691e1 Protein kinase (NPK-110)
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
 ; STREET: 233 S. Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: US
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/817, 832B
 ; FILING DATE: 28-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/EP95/04258
 ; FILING DATE: 30-OCT-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 94 11 7122.5
 ; FILING DATE: 28-OCT-1994
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 779 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-817-832B-31

	Query Match	55.9%;	Score 2464;	DB 4;	Length 779;
	Best Local Similarity	64.6%;	Pred. No. 2, 1e-176;		
	Matches 510;	Conservative 82;	Mismatches 112;	Indels 86;	Gaps 15;
QY	10 TLNERDTEQPLGHL-DSKPESSKSNMIRGRNSATSA-DEOPHIGNYRLKLTIGKGNFAVK	67			
	1 TENHTSVGYGTEETHIPPTKSSSRQNI PRCRNSITSATDEQPHIGNYRLQKTIGKGNFAVK	60			
QY	68 KLARHILITGGEVAAKIIIDKTQUNSSSIQKIPREPRIRINKVLNHPYIVLVLFETIEKTKLYL	127			
	61 KLAHVLTGGEVAAKIIIDKTQUNPSTIQKIFREYRIKILINHPYIVLVLFETIEKTKLYL	120			
QY	128 VMEYASGGEFVDYLVAHGRRMKEKEARAKPPOVSAVOYCHQKIFVHRDLKAENILLDADM	187			
	121 VMEYASGGEFVDYLVAHGRRMKEKEARAKPFOYSAVOYCHQKILVHRDLKAENILLDADM	180			
QY	188 NIKIADGFNSNEFTFGNKLDTPCGSPYPAALPELFGQKKYDGPEDVNSGLVILYTLTVSGS	247			

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Db      181 NIKIADFSGSNEFTGNKLDTFCCSPPYAADELQKKYDDEPDVWMSLGIYLTIVSGS 240
Qy      248 LPFGQNLKEIRER-VLGRKTRIPYMSDCEMLKFLINPSKRGTELOIMDRMNV 306
Db      241 LPFGQNLKEIRER-VLGRKTRIPYMSDCEMLKFLINPSKRGTELOIMDRMNV 300
Qy      307 GHEDELCPYVEP-PDYKDPRTTELMSMGYTRREIODSLVQGRYNEVMAITYLLIGKSS 366
Db      301 GHEDELCPYVEP-PDYKDPRTTELMSMGYTRREIODSLVQGRYNEVMAITYLLIGKSS 360
Qy      367 ELEG-----DTILKPPPSADLTNSSAPSPSH-KVQRVSANPKORRFSDOAPAIPTS 419
Db      361 EFEGGESLSSGNLCQSRSPSSDLNNSTLQSPALHKNVQRTISANQKQRFSDHAGPSIRPA 420
Qy      420 NSYKKTQSNNAENKREPE-DRESGRKASST-----AKVPASPLPGLERKKTTPSTNS 473
Db      421 VSYKRPDANSVEEQKEEMDKDTARRLGSTTVGSKSEVTASPLVGPDRKKSAGPS-NN 479
Qy      474 VLSTSTNRSPPLERASLGQASIQNGKDS-----504
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Qy      505 -----TAP-----ORVPASPSAHNISSGGAPDRTNFPRGVSS 538
Db      540 KSMSTSGHPIKVTLPTTKDGEAYRPGTAQRVPASPSAHSISAS--TPDRTFPPRGSSS 597
Qy      539 RSTFHAGOLQVRQOOLPYGVTPASPS-----GHSQORAGASGSIFSKFTSKVRRRLNE 594
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Qy      595 PESKDRVETLRPHVVGSGNDKEKEEFREAPKPSLRFTWGMKTTSMEPMKREIRKYL 654
Db      655 GEASGRDTRAR---GSSGEPKQKEGKAKPR-LRTWGMKTTSMDPRDMVREIRKYL 709
Qy      655 DANCOSSELEHKYMLCMHGTFGHEDVQWEMEVCKLPRLSLNGVRFKRISGTSMAPKNI 714
Db      710 DANCDEOREERFLFCVHDADQDSLQWEMEVCKLPRLSLNGVRFKRISGTISIAFKNI 769
Qy      715 ASKIANELKL 724
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RESULT 13
US-08-677-298-2
; Sequence 2, Application US/08677298
; Patent No. 5863729
; GENERAL INFORMATION:
; APPLICANT: Pivnica-Worms, Helen
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAR-1
; TITLE OF INVENTION: KINASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,298
; FILING DATE: 09-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 9-96

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-677-298-2

Query Match      64.2%; Score 2399; DB 2; Length 729;
Best Local Similarity 66.3%; Pred. No. 1,4e-171;
Matches 503; Conservative 73; Mismatches 115; Indels 68; Gaps 18;

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Qy      58 TTGKGNPAVKLAHHILTGKEVAVKIDKTQANSSSLQKLPRVRIMVYLNHPNIVKLPFE 117
Db      61 TTGKGNPAVKLAHHILTGREVAIKIDKTQANPSTLQKLPRVRIIMKILNHPNIVKLPFE 120
Qy      118 VIETEKTYLYLMEVYSGSEVFDYLVAGRMKEKEARFQVVSAYQVCHQKFIYHRDLK 177
Db      121 VIETEKTYLYLMEVYSGSEVFDYLVAGRMKEKEARFQVVSAYQVCHQKFIYHRDLK 180
Qy      178 AENLLDADMNKIADFGPSNEFTGNKLDTFCCSPPYAADELQKKYDDEPDVWMSLG 237
Db      181 AENLLDADMNKIKIADFGPSNEFTVGGKLDTFCCSPPYAADELQKKYDDEPDVWMSLG 240
Qy      238 VLYLYTVSGSLPFDQNLKEIRERVLGRKRYIIPYMSDCEMLKFLINPSKRGTELO 297
Db      241 VLYLYTVSGSLPFDQNLKEIRERVLGRKRYIIPYMSDCEMLKFLINPSKRGTELO 300
Qy      298 IMKDRMNVGHEDELKPYVEPLPDYKDPRTTELMSMGYTRREIODSLVQGRYNEVMAIT 357
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Qy      358 YLLIGKSSSELEBQDIT-----LKPPASADLTNSAPSPSHKVQSVSANPKORRPSD 410
Db      361 YLLIGKSSSELEBQDIT-----LKPPASADLTNSAPSPSHKVQSVSANPKORRPSD 420
Qy      411 OAGPAIPTNSGYSKKTQSNNAENKRPEDRESGRKASTAK-----VPASPLPG----- 459
Db      421 HAGPAIPSVAYIPKKSQSTADGDL-KEDGISRSKSSGSAVGGGIAIPASPMLGASNP 479
Qy      460 -----LERKKTTPSTNSVLSTSTNRSPPLERASLGQAS-IQNGKQ-STAP-QRVVPV 512
Db      480 KADIPERKKSSTVPSNSTASGAMTRRN-TYVCSERTTADRSVLQNGKENSITIDQRTPV 538
Qy      513 ASPSAHNSSSGGAPDRNPFQVSSNSTFPAQOLRQVDOQNLPGYVTPASPS-GH--- 568
Db      539 A--STHSISSA-AAPPDRIRFPFGTASSTFG---QPRERRITYNGPPASPSLSHEAT 591
Qy      569 --SQRGASSTISKFTSKFVR-RNINPEPSKDRVETLRPHVVGSGNDKEKEEFREAK 625
Db      592 PLSQTRKSGSTNLSKLTSTKTRSNVSA-----EQKQENREAK 630
Qy      626 PRSLRFTWGMKTTSMEPMKREIRKYLDAVNSCOSSELEHKYMLCMHGTFGHEDPVQWE 685
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US-09-523-849-33
; Sequence 33, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:

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QY 633 WSMKTTSSMBPNEMWREIRKVL DANCQSEIHEKYM LCMHGT PGHEDFVQWEMEVCKLP 692
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Db 693 RLSLNGVRFFKRISGTSIAFKNIASKIANELKT 724

Search completed: February 26, 2005, 17:52:59
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:51:28 / Search time 138 Seconds

(without alignments)
1721.045 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737
Sequence: 1 MSARPTPLPTLNRDTEQPT.....SGTSMFKNIASKIANKLKL 724

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3737	100.0	724	US-10-274-194-2	Sequence 2, Appl1
2	3737	100.0	724	US-10-760-407-2	Sequence 2, Appl1
3	3736	100.0	724	US-09-919-585-9	Sequence 9, Appl1
4	3670.5	98.2	787	US-10-618-941-76	Sequence 76, Appl1
5	3654	97.8	722	US-10-764-194-4	Sequence 4, Appl1
6	3654	97.8	722	US-10-760-407-4	Sequence 4, Appl1
7	3644	97.5	722	US-08-817-8328-32	Sequence 32, Appl1
8	3644	97.5	722	US-10-440-435-32	Sequence 32, Appl1
9	3566	95.4	691	US-09-919-585-6	Sequence 6, Appl1
10	3515	94.1	745	US-10-195-101-36	Sequence 36, Appl1
11	3515	94.1	745	US-10-161-565-24	Sequence 24, Appl1
12	3515	94.1	745	US-10-260-708-79	Sequence 79, Appl1
13	2555	68.4	793	US-10-195-101-32	Sequence 32, Appl1

14	2552	68.3	795	9	US-09-919-585-12	Sequence 12, Appl1
15	2552	68.3	795	15	US-10-311-034-4	Sequence 4, Appl1
16	2552	68.3	795	17	US-10-753-267-120	Sequence 120, Appl1
17	2546	68.1	795	14	US-10-142-356-9	Sequence 9, Appl1
18	2546	68.1	795	14	US-10-161-565-25	Sequence 25, Appl1
19	2464	65.9	779	8	US-08-817-8328-31	Sequence 31, Appl1
20	2464	65.9	779	15	US-10-440-435-31	Sequence 31, Appl1
21	2419.5	64.7	744	9	US-09-919-585-3	Sequence 3, Appl1
22	2399.5	64.2	744	9	US-09-835-081-4	Sequence 4, Appl1
23	2399	64.2	729	14	US-10-142-356-11	Sequence 11, Appl1
24	2399	64.2	729	14	US-10-195-101-33	Sequence 33, Appl1
25	2399	64.2	729	14	US-10-161-565-26	Sequence 26, Appl1
26	2395.5	64.1	776	15	US-10-366-288-6	Sequence 6, Appl1
27	2381	63.7	713	14	US-10-161-565-27	Sequence 27, Appl1
28	2308	61.8	667	15	US-10-016-248-74	Sequence 74, Appl1
29	2163	57.9	749	15	US-10-333-314-8	Sequence 8, Appl1
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31	1940.5	51.9	752	15	US-10-258-106-16	Sequence 16, Appl1
32	1940.5	51.9	752	15	US-10-276-645-7	Sequence 7, Appl1
33	1940.5	51.9	825	15	US-10-425-114-54516	Sequence 54516, A
34	1936.5	51.8	752	16	US-10-618-941-79	Sequence 79, Appl1
35	1925	51.5	769	15	US-10-363-616-403	Sequence 403, Appl1
36	1913.5	51.2	724	15	US-10-276-645-5	Sequence 5, Appl1
37	1908	51.1	703	15	US-10-016-248-70	Sequence 70, Appl1
38	1878.5	50.3	638	14	US-10-059-585-8	Sequence 8, Appl1
39	1814.5	48.6	698	15	US-10-016-248-22	Sequence 22, Appl1
40	1771	47.4	1038	15	US-10-424-599-274878	Sequence 274878, A
41	1721.5	46.1	688	15	US-10-276-645-8	Sequence 8, Appl1
42	1713.5	45.9	688	14	US-10-161-565-28	Sequence 28, Appl1
43	1713.5	45.9	688	14	US-10-161-565-29	Sequence 29, Appl1
44	1707	45.7	1246	15	US-10-369-493-6585	Sequence 6585, Appl1
45	1693.5	45.3	660	15	US-10-276-645-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-274-194-2
Sequence 2, Application US/10274194
Publication No. US20030232408A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C1001306DIV
CURRENT APPLICATION NUMBER: US/10/274,194
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 724
TYPE: PRT
ORGANISM: Homo sapiens
US-10-274-194-2

Query Match 100.0%; Score 3737; DB 15; Length 724;
Best Local Similarity 100.0%; Pred. No. 1.9e-220;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db

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1 MSARPTPLPTLNRDTEQPTLGHLDSPKSKNMINGRNSATSDADQPHGNTRLKTTIG 60

QY 61 KGNFAVKLARHILTGKEVAVKIIDKTQLNSSLQKLPREVRIMKVLNHPNIYKLVFVIE 120
61 KGNFAVKLARHILTGKEVAVKIIDKTQLNSSLQKLPREVRIMKVLNHPNIYKLVFVIE 120

QY 121 TEKTLVLYNEVYSGGEVFDVLVHGRMKEKARAKROVSAVOYCHQKRTIYHRDLKAEN 180
121 TEKTLVLYNEVYSGGEVFDVLVHGRMKEKARAKROVSAVOYCHQKRTIYHRDLKAEN 180

Db

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Db      241  YTLVSSGLPFDGQNLPELREERVLRGKYRIPEWYSTOCENLLKKFLLINBSKGTLEQINK 300
QY      301  DEWMNVGHEDELKPYVEPLPDYKDBRTLELWWSMGYTRBEEIDSLVQGRYNEVWATYLL 360
Db      301  DEWMNVGHEDELKPYVEPLPDYKDBRTLELWWSMGYTRBEEIDSLVQGRYNEVWATYLL 360
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Db      361  LGYKSELEGGDTTLTKPRPSADLTNSASPSHKYQRYSANPKORFSDQAPALPTSN 420
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QY      661  SEIHEKTMLLCMHGTPGHEDPVQWMEVCKLPRLSLNGYRFRIGTSMAFNIAKIAN 720
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QY      721  ELKL 724
Db      721  ELKL 724

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; Sequence 2, Application US/10760407
; Publication No. US20040137499A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C0001306-DIV II
; CURRENT APPLICATION NUMBER: US/10/760,407
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-760-407-2

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Db	301	DEMMNVGHEDDLKRYVEPLDYKDPBRTLELVSMGTYRBEIODSLVGORVNEWMATYLL	360
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Db	361	LGKXSELEGDITTLKPRPSADLTJNSSAPSFSHKYORSANPKORPFSDDQAPLPTSN	420
QY	421	SYSKTQOSNNAENKKPEEDRESGRKASSTAKVPASPLPGLERKTTPTPSTNSVLSTSTN	480
Db	421	SYSKTQOSNNAENKKPEEDRESGRKASSTAKVPASPLPGLERKTTPTPSTNSVLSTSTN	480
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QY	541	TFHAGOLRQVNDQNLPGVTPPASPSPGSGOGRGASGISFSKFTSKFYVRNINPEESKDR	600
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QY	601	VETLRPHNVGSGGNDKEKEEFREAPRSLRFTWSKTTSSMEPNMMEIRKVLVDANSQ	660
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Db	661	SELHEKYMLLCMHGTPGHEDEVQWEMEVCSKLPRLSLNGVRFPKRISGTSMAFNKIASKIAN	720
QY	721	ELKTL 724	
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RESULT 3
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; Sequence 9, Application US/09919585
; Patent No. US20020115167A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Tian-Qiang
; APPLICANT: Feng, Jia-Jia
; APPLICANT: Reinhard, Christoph
; APPLICANT: Fantl, Wendy J.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING PAR-1
; TITLE OF INVENTION: POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZ
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: PP-016093.002/200130.525
; CURRENT APPLICATION NUMBER: US/09/919,585
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ. ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-585-9

Query Match      100.0%; Score 3736; DB 9; Length 724;
Best Local Similarity 99.9%; Pred. No. 2,2e-220;
Matches 723; Conservative 1; Mismatches 0;
Indels 0; Gaps 0;

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Db      61  KGNPAKYLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNHNHNYVLFEVIE 120
Qy      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVSVOYCHQKFIVHDLKAEN 180
      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVSVOYCHQKFIVHDLKAEN 180
Db      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVSVOYCHQKFIVHDLKAEN 180
Qy      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAAPBLFQKKYDGPEDVWSLGVTIL 240
      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAAPBLFQKKYDGPEDVWSLGVTIL 240
Db      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAAPBLFQKKYDGPEDVWSLGVTIL 240
Qy      241  YTLVSGSLPFDGQNLKELRERVLRGKYRIPFVMSDCEMLKKFLILNPSKRGTLBQIMK 300
      241  YTLVSGSLPFDGQNLKELRERVLRGKYRIPFVMSDCEMLKKFLILNPSKRGTLBQIMK 300
Db      241  YTLVSGSLPFDGQNLKELRERVLRGKYRIPFVMSDCEMLKKFLILNPSKRGTLBQIMK 300
Qy      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIIDSILVGQRYNEVMATYLL 360
      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIIDSILVGQRYNEVMATYLL 360
Db      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIIDSILVGQRYNEVMATYLL 360
Qy      361  LDYKSELGDDTTLKPRPSADLTNSAPSPSHKVORSVANPKQRFPDQAGPALFTSN 420
      361  LDYKSELGDDTTLKPRPSADLTNSAPSPSHKVORSVANPKQRFPDQAGPALFTSN 420
Db      361  LDYKSELGDDTTLKPRPSADLTNSAPSPSHKVORSVANPKQRFPDQAGPALFTSN 420
Qy      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTN 480
      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTN 480
Db      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTN 480
Qy      481  RSRNSPLLEBASLGQASIQNGKOSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRS 540
      481  RSRNSPLLEBASLGQASIQNGKOSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRS 540
Db      481  RSRNSPLLEBASLGQASIQNGKOSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRS 540
Qy      541  TFAAGQLRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFVRNLNPEPEKDR 600
      541  TFAAGQLRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFVRNLNPEPEKDR 600
Db      541  TFAAGQLRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFVRNLNPEPEKDR 600
Qy      601  VFTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 660
      601  VFTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 660
Db      601  VFTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 660
Qy      661  SFHEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
      661  SFHEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
Db      661  SFHEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 720
Qy      721  ELKL 724
      721  ELKL 724
Db      721  ELKL 724

```

```

RESULT 4
US-10-618-941-76
; Sequence 76, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: MAYTE, DAVID
; APPLICANT: MANNING, GERRARD
; APPLICANT: CAENEPEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618, 941
; PRIORITY FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395, 632
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 787
; TYPE: PRF
; ORGANISM: Homo sapiens

```

```

US-10-618-941-76
Query Match      98.2%; Score 3670.5; DB 16; Length 787;
Best Local Similarity 91.6%; Pred. No. 2,56-216;
Matches 721; Conservative 1; Mismatches 2; Indels 63; Gaps 2;

Qy      1  MSARPTPLTNERDTEQPTLGHLDSPKSSKSNMIRGNATSADDEQPHIGNRLLKTTIG 60
      1  MSARPTPLTNERDTEQPTLGHLDSPKSSKSNMIRGNATSADDEQPHIGNRLLKTTIG 60
Db      1  MSARPTPLTNERDTEQPTLGHLDSPKSSKSNMIRGNATSADDEQPHIGNRLLKTTIG 60
Qy      61  KGNPAKYLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNHNHNYVLFEVIE 120
      61  KGNPAKYLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNHNHNYVLFEVIE 120
Db      61  KGNPAKYLARHILITGKEVAVKIIDKTQUNSSSIQKLFREVRIMKVLNHNHNYVLFEVIE 120
Qy      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVSVOYCHQKFIVHDLKAEN 180
      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVSVOYCHQKFIVHDLKAEN 180
Db      121  TEKTLVYMEYASGGEVFDYLVAGRMKEKAKAFQVAVSVOYCHQKFIVHDLKAEN 180
Qy      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAAPBLFQKKYDGPEDVWSLGVTIL 240
      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAAPBLFQKKYDGPEDVWSLGVTIL 240
Db      181  LLLDADNNIKIADGFSNEFTFGNKLDTFCGSPPYAAPBLFQKKYDGPEDVWSLGVTIL 240
Qy      241  YTLVSGSLPFDGQNLKELRERVLRGKYRIPFVMSDCEMLKKFLILNPSKRGTLBQIMK 300
      241  YTLVSGSLPFDGQNLKELRERVLRGKYRIPFVMSDCEMLKKFLILNPSKRGTLBQIMK 300
Db      241  YTLVSGSLPFDGQNLKELRERVLRGKYRIPFVMSDCEMLKKFLILNPSKRGTLBQIMK 300
Qy      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIIDSILVGQRYNEVMATYLL 360
      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIIDSILVGQRYNEVMATYLL 360
Db      301  DRMMNVGHEDDELKPYVEPLPDYKDPRRTELAMVSMGYTREIIDSILVGQRYNEVMATYLL 360
Qy      361  LDYKSELGDDTTLKPRPSADLTNSAPSPSHKVORSVANPKQRFPDQAGPALFTSN 420
      361  LDYKSELGDDTTLKPRPSADLTNSAPSPSHKVORSVANPKQRFPDQAGPALFTSN 420
Db      361  LDYKSELGDDTTLKPRPSADLTNSAPSPSHKVORSVANPKQRFPDQAGPALFTSN 420
Qy      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTN 480
      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTN 480
Db      421  SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSTSTN 480
Qy      481  RSRNSPLLEBASLGQASIQNGKOSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRS 540
      481  RSRNSPLLEBASLGQASIQNGKOSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRS 540
Db      481  RSRNSPLLEBASLGQASIQNGKOSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRS 540
Qy      504  -----STPDRVPVAPSAHNISSSGGAADRTPNPRGVSSRSSTPFAQ 546
      504  -----STPDRVPVAPSAHNISSSGGAADRTPNPRGVSSRSSTPFAQ 546
Db      541  KASGLPEPTSENCVPPSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRSSTPFAQ 600
      541  KASGLPEPTSENCVPPSTAPQRPVAPSAHNISSSGGAADRTPNPRGVSSRSSTPFAQ 600
Qy      547  LRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFV-----RRNLNPEPS 597
      547  LRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFV-----RRNLNPEPS 597
Db      601  LRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFVRNLNPEPEKDR 660
      601  LRQVRDQONLPYGVTPPASPSGHSQGRGASGSIFFSKFTSKFVRNLNPEPEKDR 660
Qy      598  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 657
      598  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 657
Db      661  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 720
      661  KDRVETLRPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPEMMREIRKVLNANSCQ 720
Qy      658  SCQSELEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 717
      658  SCQSELEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 717
Db      721  SCQSELEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 780
      721  SCQSELEHEKMYLGMGTGHEHPVQWEMEVCLPRLSLNGVRFKRIISGTSMAFKNIASKIAN 780
Qy      718  IANELKL 724
      718  IANELKL 724
Db      781  IANELKL 787

```

```

RESULT 5
US-10-274-194-4
; Sequence 4, Application US/10274194
; Publication No. US20030322408A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV

```



```
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PR
; ORGANISM: Rattus norvegicus
US-10-274-194-4
```

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Query Match      97.8%; Score 3654; DB 15; Length 722;
Best Local Similarity 97.8%; Pred. No. 2.3e-215;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
```

```
QY      1 MSSARTPLPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNTYRLKTTIG 60
DB      1 MSSARTPLPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNTYRLKTTIG 60
QY      61 KGNFAKVLARHILTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHNPIVKLFVIE 120
DB      61 KGNFAKVLARHILTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHNPIVKLFVIE 120
QY      121 TEKTYLIMEVYASGGEVFDYLVAGRMKEKEARAFQVSAVOYCHQKFIYHRDLKAEN 180
DB      121 TEKTYLIMEVYASGGEVFDYLVAGRMKEKEARAFQVSAVOYCHQKFIYHRDLKAEN 180
QY      181 LLLDADNMIKIADFGSNEFTFGNKLDFPGSPPYAAPELQGGKYDDEVDVWSLGVIL 240
DB      181 LLLDADNMIKIADFGSNEFTFGNKLDFPGSPPYAAPELQGGKYDDEVDVWSLGVIL 240
QY      241 YTLVSGSLPFDQNLKELREYLRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
DB      241 YTLVSGSLPFDQNLKELREYLRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
QY      301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
DB      301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
QY      361 LGYKSELEGGDTITLKRPSPADLTNSAPSPSHKVSANPKORRSPDOAGPAIPTSN 420
DB      361 LGYKSELEGGDTITLKRPSPADLTNSAPSPSHKVSANPKORRSPDOAGPAIPTSN 420
QY      421 SYSKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLERKKTTPTESTNSVLSTSTN 480
DB      421 SYSKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLERKKTTPTESTNSVLSTSTN 480
QY      481 RSRNSPLLEBASLGQASIQNGKDSAPQVPAVPSAHNITSSGGAAPDRTNFRGVSSRS 540
DB      481 RSRNSPLLEBASLGQASIQNGKDSAPQVPAVPSAHNITSSGGAAPDRTNFRGVSSRS 540
QY      541 TFHAGOLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSKEFTSKFYVRNLNPESSKDR 600
DB      541 TFHAGOLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSKEFTSKFYVRNLNPESSKDR 600
QY      599 VETLRPHVVGSGGSDTDEKEEFREAKPRSLRFTWSMKTSSMEPEMREIRKVLDA NSCQ 658
DB      599 VETLRPHVVGSGGSDTDEKEEFREAKPRSLRFTWSMKTSSMEPEMREIRKVLDA NSCQ 658
QY      661 SELHEKYVLLCMGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASXIAN 720
DB      661 SELHEKYVLLCMGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASXIAN 720
QY      721 ELKTL 724
DB      719 ELKTL 722
```

```
RESULT 6
US-10-760-407-4
; Sequence 4, Application US/10760407
; Publication No. US20040137499A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
```

```
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01306-DIV II
; CURRENT APPLICATION NUMBER: US/10/760,407
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PR
; ORGANISM: Rattus norvegicus
US-10-760-407-4
```

```
Query Match      97.8%; Score 3654; DB 16; Length 722;
Best Local Similarity 97.8%; Pred. No. 2.3e-215;
Matches 708; Conservative 9; Mismatches 5; Indels 2; Gaps 1;
```

```
QY      1 MSSARTPLPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNTYRLKTTIG 60
DB      1 MSSARTPLPTLNEDTQPTLGHLDSPSSKSNMIRGNATSADDEPHIGNTYRLKTTIG 60
QY      61 KGNFAKVLARHILTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHNPIVKLFVIE 120
DB      61 KGNFAKVLARHILTGKEVAVKIIDKTQUNSSSLQKLFREVRIMKVLNHNPIVKLFVIE 120
QY      121 TEKTYLIMEVYASGGEVFDYLVAGRMKEKEARAFQVSAVOYCHQKFIYHRDLKAEN 180
DB      121 TEKTYLIMEVYASGGEVFDYLVAGRMKEKEARAFQVSAVOYCHQKFIYHRDLKAEN 180
QY      181 LLLDADNMIKIADFGSNEFTFGNKLDFPGSPPYAAPELQGGKYDDEVDVWSLGVIL 240
DB      181 LLLDADNMIKIADFGSNEFTFGNKLDFPGSPPYAAPELQGGKYDDEVDVWSLGVIL 240
QY      241 YTLVSGSLPFDQNLKELREYLRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
DB      241 YTLVSGSLPFDQNLKELREYLRGKYRIPFYMSDCEMLKKFLLINPSKRGTLQIMK 300
QY      301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
DB      301 DRMMNVGHEDDELKPYVEPLDYKDPRTTELMSMGYTRREIODSLVGQRINEWATYLL 360
QY      361 LGYKSELEGGDTITLKRPSPADLTNSAPSPSHKVSANPKORRSPDOAGPAIPTSN 420
DB      361 LGYKSELEGGDTITLKRPSPADLTNSAPSPSHKVSANPKORRSPDOAGPAIPTSN 420
QY      421 SYSKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLERKKTTPTESTNSVLSTSTN 480
DB      421 SYSKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLERKKTTPTESTNSVLSTSTN 480
QY      481 RSRNSPLLEBASLGQASIQNGKDSAPQVPAVPSAHNITSSGGAAPDRTNFRGVSSRS 540
DB      481 RSRNSPLLEBASLGQASIQNGKDSAPQVPAVPSAHNITSSGGAAPDRTNFRGVSSRS 540
QY      541 TFHAGOLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSKEFTSKFYVRNLNPESSKDR 600
DB      541 TFHAGOLRQVDDQNLPGVTPPASPSGHSQGRGASGSIFSKEFTSKFYVRNLNPESSKDR 600
QY      599 VETLRPHVVGSGGSDTDEKEEFREAKPRSLRFTWSMKTSSMEPEMREIRKVLDA NSCQ 658
DB      599 VETLRPHVVGSGGSDTDEKEEFREAKPRSLRFTWSMKTSSMEPEMREIRKVLDA NSCQ 658
QY      661 SELHEKYVLLCMGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASXIAN 720
DB      661 SELHEKYVLLCMGTGPHGDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASXIAN 720
QY      721 ELKTL 724
DB      719 ELKTL 722
```

```
RESULT 7
US-08-817-832B-32
```

```

; Sequence 32, Application US/08817832B
; Publication No. US20030104516A1
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. US20030104516A1 Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-817-832B-32

```

Query Match 97.5%; Score 3644; DB 8; Length 722;

Best local similarity 97.5%; Pred. No. 9.5e-215;

Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

```

QY 1 MSSARPLPLTNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKTTIG 60
DB 1 MSSARPLPLTNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKTTIG 60
QY 61 KGNPAKYKLARHILITGEVAVKIIDKTQNLSSSIQKLPREVRIMKVLNHPNIVKLEFVIE 120
DB 61 KGNPAKYKLARHILITGEVAVKIIDKTQNLSSSIQKLPREVRIMKVLNHPNIVKLEFVIE 120
QY 121 TEKTLVLMVEYASGGEVFDVLVAHGMRKEKARAKFRQVSAVOYCHOKFIYHRDLKAEN 180
DB 121 TEKTLVLMVEYASGGEVFDVLVAHGMRKEKARAKFRQVSAVOYCHOKFIYHRDLKAEN 180
QY 181 LLLDADNNIKIADFGFNEFTFGNKLDTFCGSPPEYAAPLFGQKKYDGPEDVWSLGVIL 240
DB 181 LLLDADNNIKIADFGFNEFTFGNKLDTFCGSPPEYAAPLFGQKKYDGPEDVWSLGVIL 240
QY 241 YTLVSGSLPFDGQNLKELREVRILGKRIIPYWSSTDCENLIKFLIINPSKRGTLBQIMK 300
DB 241 YTLVSGSLPFDGQNLKELREVRILGKRIIPYWSSTDCENLIKFLIINPSKRGTLBQIMK 300
QY 301 DRMMNVGHEDDELKPYEPLPDYKDPRTLELMSVGTREIIDSILVGOYVNEVMATYLL 360
DB 301 DRMMNVGHEDDELKPYEPLPDYKDPRTLELMSVGTREIIDSILVGOYVNEVMATYLL 360
QY 361 LGYKSSLEEDDTITLKRPSPADLTNSAPSPSHKVCVSVANPKQRHFSQAGPAIPTSN 420
DB 361 LGYKSSLEEDDTITLKRPSPADLTNSAPSPSHKVCVSVANPKQRHFSQAGPAIPTSN 420
QY 421 SYGKTKOSNNAENKRPEDRSKASTAKVNPASPLPGLEBKKTTPPTSTNSVLTSTN 480
DB 421 SYGKTKOSNNAENKRPEDRSKASTAKVNPASPLPGLEBKKTTPPTSTNSVLTSTN 480
QY 481 RSRNSPLLEBASLGQASIQNGKOSTAFQRPVVASPSAHNITSSSGGADRNPFGVSSRS 540

```

```

DB 479 RSRNSPLLEBASLGQASIQNGKOSTAFQRPVVASPSAHNITSSSGGADRNPFGVSSRS 538
QY 541 TFHAGQLROYRDOONLPEYVTTPASPSGSGRRGASGIFSFKPTSKFVRRLNLPSSKDR 600
DB 539 TFHAGQLROYRDOONLPEYVTTPASPSGSGRRGASGIFSFKPTSKFVRRLNLPSSKDR 598
QY 601 VETLRPRVVGSGNDKEKEFRFAKPRSLAFTVSMKTTSSMEPEVMREIRKVLDA NSCQ 660
DB 599 VETLRPRVVGSGNDKEKEFRFAKPRSLAFTVSMKTTSSMEPEVMREIRKVLDA NSCQ 658
QY 661 SELHEKYMILCMHGTPEGHEDFVQWEMEVCKLPRLSLNGVFPKRIISGTMFAKNYASXTAN 720
DB 659 SELHEKYMILCMHGTPEGHEDFVQWEMEVCKLPRLSLNGVFPKRIISGTMFAKNYASXTAN 718
QY 721 ELKL 724
DB 719 ELKL 722

```

RESULT 8

US-10-440-435-32

; Sequence 32, Application US/10440435

; Publication No. US20040038361A1

; GENERAL INFORMATION:

; APPLICANT: MANDELKOW, Eckhard, et al.

; TITLE OF INVENTION: No. US20040038361A1 Protein Kinase (NPK-110)

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 233 S. Wacker Drive, 6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

; COUNTRY: US

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/440,435

; FILING DATE: 16-May-2003

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/EP95/04258

; FILING DATE: 30-OCT-1995

; APPLICATION NUMBER: EP 94 11 7122.5

; FILING DATE: 28-OCT-1994

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 722 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-440-435-32

Query Match 97.5%; Score 3644; DB 15; Length 722;

Best local similarity 97.5%; Pred. No. 9.5e-215;

Matches 706; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

```

QY 1 MSSARPLPLTNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKTTIG 60
DB 1 MSSARPLPLTNERDTEOPTLGHLDSPSSKSNMIRGNSATSADQPHIGNYRLKTTIG 60
QY 61 KGNPAKYKLARHILITGEVAVKIIDKTQNLSSSIQKLPREVRIMKVLNHPNIVKLEFVIE 120
DB 61 KGNPAKYKLARHILITGEVAVKIIDKTQNLSSSIQKLPREVRIMKVLNHPNIVKLEFVIE 120
QY 121 TEKTLVLMVEYASGGEVFDVLVAHGMRKEKARAKFRQVSAVOYCHOKFIYHRDLKAEN 180
DB 121 TEKTLVLMVEYASGGEVFDVLVAHGMRKEKARAKFRQVSAVOYCHOKFIYHRDLKAEN 180

```

QY 181 LLLDADNMNLIKADFGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGEVDVMSLVIL 240
DB 181 LLLDADNMNLIKADFGFSNEFTFGNKLDTFCGSPPYAABELFOGKKYDGEVDVMSLVIL 240
QY 241 YTLVSGSLPFDGQNLKELRERVLKQRYRIPFYMSTDCENLLKPELILNPSKRGTLQOIMK 300
DB 241 YTLVSGSLPFDGQNLKELRERVLKQRYRIPFYMSTDCENLLKPELILNPSKRGTLQOIMK 300
QY 301 DRMNNGHEDEKLPYVEPLPDYDPRTELMVSMGTREIQLSLVGQRYNEVMAVYLL 360
DB 301 DRMNNGHEDEKLPYVEPLPDYDPRTELMVSMGTREIQLSLVGQRYNEVMAVYLL 360
QY 361 LGYSSELEGGDTTLTKRPSADLTNSAPSPSHVQSVSANPKQRRFSDQAGPATPTSN 420
DB 361 LGYSSELEGGDTTLTKRPSADLTNSAPSPSHVQSVSANPKQRRFSDQAGPATPTSN 420
QY 421 SYSKTOSNNANENKRPEDRESGRKASTAKVPAPLPGLERKKTPTPTSTNSVLTSTN 480
DB 421 SYSKTOSNNANENKRPEDRESGRKASTAKVPAPLPGLERKKTPTPTSTNSVLTSTN 480
QY 481 RSRNSPLERASIGQASTIQNGKDTAPQRPVAPSPSAHNTSSSGADRTNPRGVSRS 540
DB 479 RSRNSPLERASIGQASTIQNGKDTAPQRPVAPSPSAHNTSSSGADRTNPRGVSRS 538
QY 541 TFHAGQLROYDQONLPGYVTPASPSSGSGRGAAGSIFSKFTSKFVRNLNPEBKDR 600
DB 539 TFHAGQLROYDQONLPGYVTPASPSSGSGRGAAGSIFSKFTSKFVRNLNPEBKDR 598
QY 601 VETLRPHVVGSGGNDKEKEEFREAKPRSLRPTWSMKTTSMEPMEMREIRKVLANSQC 660
DB 599 VETLRPHVVGSGGNDKEKEEFREAKPRSLRPTWSMKTTSMEPMEMREIRKVLANSQC 658
QY 661 SELHEKTMLCMHGTPEHEDPVQWEMEVCKLPRLSLNGVRFKRLSGTSMAFKNIASKIAN 720
DB 659 SELHEKTMLCMHGTPEHEDPVQWEMEVCKLPRLSLNGVRFKRLSGTSMAFKNIASKIAN 718
QY 721 ELKLI 724
DB 719 ELKLI 722

RESULT 9
US-09-919-585-6
/ Sequence 6, Application US/09919585
/ Patent No. US20020115167A1
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Tian-Qiang
/ APPLICANT: Feng, Jia-Jia
/ APPLICANT: Reinhard, Christoph
/ APPLICANT: Fanti, Wendy J.
/ APPLICANT: Williams, Lewis T.
/ TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING PAR-1
/ TITLE OF INVENTION: POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZI
/ FILE REFERENCE: PP-016093.002/200130.525
/ CURRENT APPLICATION NUMBER: US/09/919,585
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 691
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-919-585-6

Query Match 95.4%; Score 3566; DB 9; Length 691;
Best Local Similarity 99.5%; Pred. No. 5.4e-210;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 34 MIRGRSATSADBPQHIGNYRLIKTIGKGNFAVKLARHLNGKEVAVKIIDKTOLNSS 93
DB 1 MIRGRSATSADBPQHIGNYRLIKTIGKGNFAVKLARHLNGKEVAVKIIDKTOLNSS 60

QY 94 LQKLPREVRIMKVLNPNVVKLPREVIETEKTYLVWEYASGGEVFPDYLVAHGMEKEAR 153
DB 61 LQKLPREVRIMKVLNPNVVKLPREVIETEKTYLVWEYASGGEVFPDYLVAHGMEKEAR 120
QY 154 AKFRQVSAVQYCHQFPIYHRDLKABNLILLDADNMNLIKADFGFSNEFTFGNKLDTFCGSP 213
DB 121 AKFRQVSAVQYCHQFPIYHRDLKABNLILLDADNMNLIKADFGFSNEFTFGNKLDTFCGSP 180
QY 214 PYAAPLFOGKKYDGEVDVMSLVILYTLVSGSLPFDGQNLKELRERVLKQRYRIPFYM 273
DB 181 PYAAPLFOGKKYDGEVDVMSLVILYTLVSGSLPFDGQNLKELRERVLKQRYRIPFYM 240
QY 274 STDCEMLKKPELILNPSKRGTLQOIMKQRMNVGHEDDLKPYVEPLPDYDPRTELMV 333
DB 241 STDCEMLKKPELILNPSKRGTLQOIMKQRMNVGHEDDLKPYVEPLPDYDPRTELMV 300
QY 334 SMGTYREELQDSLVGQRYNEVMAVYLLLGYSSELEGGDTTLTKRPSADLTNSAPSPSH 393
DB 301 SMGTYREELQDSLVGQRYNEVMAVYLLLGYSSELEGGDTTLTKRPSADLTNSAPSPSH 360
QY 394 KYQRSYSANPKQRRPSDQAGPALPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 453
DB 361 KYQRSYSANPKQRRPSDQAGPALPTNSYSKKTQSNNAENKRPEDRESGRKASTAKVP 420
QY 454 ASPLPELERKKTPTPTSTNSVLTSTNBSRNPILERASIGQASTIQNGKDTAPQRPVAP 513
DB 421 ASPLPELERKKTPTPTSTNSVLTSTNBSRNPILERASIGQASTIQNGKDTAPQRPVAP 480
QY 514 SPSAHNTSSSGGAPDRTNPRGVSSRSTFHAGQLROYDQONLPGYVTPASPSSGSGR 573
DB 481 SPSAHNTSSSGGAPDRTNPRGVSSRSTFHAGQLROYDQONLPGYVTPASPSSGSGR 540
QY 574 GASGSIFSKFTSKFVRNLNPEBKDRVETLRPHVVGSGGNDKEKEEFREAKPRSLRPTW 633
DB 541 GASGSIFSKFTSKFVRNLNPEBKDRVETLRPHVVGSGGNDKEKEEFREAKPRSLRPTW 600
QY 634 SMKTTSMEPMEMREIRKVLANSQSELEHKYVLLCMHGTPEHEDPVQWEMEVCKLP 693
DB 601 SMKTTSMEPMEMREIRKVLANSQSELEHKYVLLCMHGTPEHEDPVQWEMEVCKLP 660
QY 694 ISLNGVRFKRLSGTSMAFKNIASKIANELK 724
DB 661 ISLNGVRFKRLSGTSMAFKNIASKIANELK 691

RESULT 10
US-10-195-101-36
/ Sequence 36, Application US/10195101
/ Publication No. US20030087317A1
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Molteni, Angela
/ APPLICANT: Magnaghi, Paola
/ APPLICANT: Bosotti, Roberta
/ APPLICANT: Scaccheri, Emanuela
/ APPLICANT: Isacchi, Antonella
/ APPLICANT: Hodgson, David M.
/ TITLE OF INVENTION: HUMAN NIM1 KINASE
/ FILE REFERENCE: PC-0009-1 CIP
/ CURRENT APPLICATION NUMBER: US/10/195,101
/ PRIOR APPLICATION DATE: 2002-07-11
/ PRIOR APPLICATION NUMBER: 09/523,849
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PERT Program
/ SEQ ID NO 36
/ LENGTH: 745
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc feature
/ OTHER INFORMATION: GenBank Accession No. US20030087317A1 g1749794

DATABASE ENTRY DATE: 1 October 1998
US-10-195-101-36

Query Match 94.1%; Score 3515; DB 14; Length 745;
Best Local Similarity 92.3%; Pred. No. 7.8e-207;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY 34 MINGRNSATSADBPPIGNRLIKTIGKNPAKYKLARHILITGKEVAVKIIDKTQNLSSS 93
DB 1 MINGRNSATSADBPPIGNRLIKTIGKNPAKYKLARHILITGKEVAVKIIDKTQNLSSS 60
QY 94 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKKEAR 153
DB 61 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKKEAR 120
QY 154 AKRQVSAVOYCHQKFIYHRDLKAENLLDADNIIKIADFGFSNEFTFGNKLDTFCGSP 213
DB 121 AKRQVSAVOYCHQKFIYHRDLKAENLLDADNIIKIADFGFSNEFTFGNKLDTFCGSP 180
QY 214 PYAAPBELFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIPIFYM 273
DB 181 PYAAPBELFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIPIFYM 240
QY 274 STDCENLKKKFLILNPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 333
DB 241 STDCENLKKKFLILNPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 300
QY 334 SMGYTBEIIDSIVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 393
DB 301 SMGYTBEIIDSIVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 360
QY 394 KVORSVSNPKORRFSQDAGPAIPTNSYSKKTOSNNAENKRPEDESGRKA5STAKVP 453
DB 361 KVORSVSNPKORRFSQDAGPAIPTNSYSKKTOSNNAENKRPEDESGRKA5STAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLSTSTNRSN5PLERASLGQASIQNGKD----- 503
DB 421 ASPLPGLERKKTPTPTSTNSVLSTSTNRSN5PLERASLGQASIQNGKD----- 480
QY 504 -----STAPORVPVAPSAHN 519
DB 481 TASASAASAPROROKMSASVHPNKA5GLPPTESNCEVPRPSTAPQRPVAPSAHN 540
QY 520 ISSSGGAPDRTNPRGVSSRSTFHAQLRQVRDQNLPGVTPASPSGHSQGRGASGI 579
DB 541 ISSSGGAPDRTNPRGVSSRSTFHAQLRQVRDQNLPGVTPASPSGHSQGRGASGI 600
QY 580 FSKFTSKFVRNINPEESKDRVETLARPHVVGSGNDKEEPEAKPRSLRFTWSMKTTS 639
DB 601 FSKFTSKFVRNINPEESKDRVETLARPHVVGSGNDKEEPEAKPRSLRFTWSMKTTS 660
QY 640 SMEPNEMREIRKVLNANSCQSELEHKYMLLCHGTPGHEDFVQMEVEVCKLPRLSINGV 699
DB 661 SMEPNEMREIRKVLNANSCQSELEHKYMLLCHGTPGHEDFVQMEVEVCKLPRLSINGV 720
QY 700 RPKRISGTSMAFNKIANIELKL 724
DB 721 RPKRISGTSMAFNKIANIELKL 745

RESULT 11
US-10-161-565-24
; Sequence 24, Application US/10161565
; Publication No. US20030165809A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MARKS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-086C
; CURRENT APPLICATION NUMBER: US/10/161,565
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 745
TYPE: PRF
ORGANISM: Homo sapiens
US-10-161-565-24

Query Match 94.1%; Score 3515; DB 14; Length 745;
Best Local Similarity 92.3%; Pred. No. 7.8e-207;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY 34 MINGRNSATSADBPPIGNRLIKTIGKNPAKYKLARHILITGKEVAVKIIDKTQNLSSS 93
DB 1 MINGRNSATSADBPPIGNRLIKTIGKNPAKYKLARHILITGKEVAVKIIDKTQNLSSS 60
QY 94 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKKEAR 153
DB 61 LQKLFREVRIMKVLNHPNIVKLFEVITEKTLVLMVEYASGGEVFDVLVHGRMKKEAR 120
QY 154 AKRQVSAVOYCHQKFIYHRDLKAENLLDADNIIKIADFGFSNEFTFGNKLDTFCGSP 213
DB 121 AKRQVSAVOYCHQKFIYHRDLKAENLLDADNIIKIADFGFSNEFTFGNKLDTFCGSP 180
QY 214 PYAAPBELFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIPIFYM 273
DB 181 PYAAPBELFOGKYDGPEDVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIPIFYM 240
QY 274 STDCENLKKKFLILNPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 333
DB 241 STDCENLKKKFLILNPSKGTLEQIMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELAV 300
QY 334 SMGYTBEIIDSIVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 393
DB 301 SMGYTBEIIDSIVGORYNEVMATYLLGYKSSLEBDITTLKRPASADLTNSASPSH 360
QY 394 KVORSVSNPKORRFSQDAGPAIPTNSYSKKTOSNNAENKRPEDESGRKA5STAKVP 453
DB 361 KVORSVSNPKORRFSQDAGPAIPTNSYSKKTOSNNAENKRPEDESGRKA5STAKVP 420
QY 454 ASPLPGLERKKTPTPTSTNSVLSTSTNRSN5PLERASLGQASIQNGKD----- 503
DB 421 ASPLPGLERKKTPTPTSTNSVLSTSTNRSN5PLERASLGQASIQNGKD----- 480
QY 504 -----STAPORVPVAPSAHN 519
DB 481 TASASAASAPROROKMSASVHPNKA5GLPPTESNCEVPRPSTAPQRPVAPSAHN 540
QY 520 ISSSGGAPDRTNPRGVSSRSTFHAQLRQVRDQNLPGVTPASPSGHSQGRGASGI 579
DB 541 ISSSGGAPDRTNPRGVSSRSTFHAQLRQVRDQNLPGVTPASPSGHSQGRGASGI 600
QY 580 FSKFTSKFVRNINPEESKDRVETLARPHVVGSGNDKEEPEAKPRSLRFTWSMKTTS 639
DB 601 FSKFTSKFVRNINPEESKDRVETLARPHVVGSGNDKEEPEAKPRSLRFTWSMKTTS 660
QY 640 SMEPNEMREIRKVLNANSCQSELEHKYMLLCHGTPGHEDFVQMEVEVCKLPRLSINGV 699
DB 661 SMEPNEMREIRKVLNANSCQSELEHKYMLLCHGTPGHEDFVQMEVEVCKLPRLSINGV 720
QY 700 RPKRISGTSMAFNKIANIELKL 724
DB 721 RPKRISGTSMAFNKIANIELKL 745

RESULT 12
US-10-260-708-79
; Sequence 79, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:

```

: APPLICANT: Scanlan, Matthew
: APPLICANT: Lee, Sang-Yull
: APPLICANT: Old, Lloyd
: TITLE OF INVENTION: Human Sarcoma-Associated Antigens
: FILE REFERENCE: L00461/70138
: CURRENT APPLICATION NUMBER: US/10/260,708
: CURRENT FILING DATE: 2002-09-30
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 79
: LENGTH: 745
: TYPE: PRT
: ORGANISM: homo sapiens
: US-10-260-708-79

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Query Match	94.1%;	Score 3515;	DB 15;	Length 745;
Best Local Similarity	92.3%;	Pred. No. 7.8e-207;		
Matches 688; Conservative	1;	Mismatches 2;	Indels 54;	Gaps 1;

Qy	3	MINGBNASTADADOPHIGNVRLIKTQKGNPAKVLABHLLTGKXAVAKILDKTOJNSS	93
Dp	1	MIRBNRSATSDAQPHIGNRLLKTKGNPAFVAKLAAHLLGKXAVAKILDKTOJNSS	60
Qy	94	LOKLFREVRIMKVLNHPNIVKLFVETETEKTYLVMWYSGGEVDPYVAHGRMEKBAR	15
Dp	61	LOQLFREVRIMKVLNHPNIVKLFVETETEKTYLVMWYSGGEVDPYVAHGRMEKBAR	120
Qy	154	AKFRQVSAVOYCHQKFIYHRDLKAENLLLDADMNIKIADFGFSNEFTFGNKLDTPFCSP	21
Dp	121	AKFRQIVSAVOYCHQKFIYHRDLKAENLLLDADMNIKIADFGFSNEFTFGNKLDTPFCSP	180
Qy	214	PYAPAPLFOQKRYDGEVNVMSLGVLLYTLVSGSLPFDGONIKELREVLNGKRIPEYM	240
Dp	181	PYAPAPLFOQKRYDGEVNVMSLGVLLYTLVSGSLPFDGONIKELREVLNGKRIPEYM	240
Qy	274	STDCENLLKFKELLINRSKGTLEQIMKDMNVMVGHEDDELKRYVEPLDYDOPRTTELNV	330
Dp	241	STDCENLLKFKELLINRSKGTLEQIMKDMNVMVGHEDDELKRYVEPLDYDOPRTTELNV	300
Qy	334	SMGYTBEEIODSLVGQRYNEVMAATYLLLGKYSSELEGDTTLKPRPSADLTNSSAPSPSH	393
Dp	301	SMGYTBEEIODSLVGQRYNEVMAATYLLLGKYSSELEGDTTLKPRPSADLTNSSAQPPSH	360
Qy	394	KYORISVANDPKORFEDDQAPALPFSNSISKTKTOSNNAENKRPEDRESGKASTAKVP	450
Dp	361	KYORISVANDPKORFEDDQAPALPFSNSISKTKTOSNNAENKRPEDRESGKASTAKVP	420
Qy	454	ASPLPGLERKKTPTPTSTNSVLTSTNNRBNPLERASLOASIQONKD-----	503
Dp	421	ASPLPGLERKKTPTPTSTNSVLTSTNNRBNPLERASLOASIQONKDSLTPGSRAS	480
Qy	504	-----STAPORPVVAPSAHN	519
Dp	481	TASASAABAAPRQHOKSMSASVHPNKASGLPTRESNCEVBRPSTAPORPVVAPSAHN	540
Qy	520	ISSGGAAPRTNPPRVSRSSTFPAQOLROYRDOONLEPYGTPPASPSSHSGRRGASGSI	579
Dp	541	ISSGGAAPRTNPPRVSRSSTFPAQOLROYRDOONLEPYGTPPASPSSHSGRRGASGSI	600
Qy	580	FSKFTSKFRRNINBESKORVETLRPHVVGSGGNDKKEEFREAKPSPSLFTMSKMTTS	639
Dp	601	FSKFTSKFRRNINBESKORVETLRPHVVGSGGNDKKEEFREAKPSPSLFTMSKMTTS	660
Qy	640	SNEPNEMWEIRKVLDAVNSCOSELHEKTYLJCMGTPGHEDFVOMENEVCKLPPLSLNGV	699
Dp	661	SNEPNEMWEIRKVLDAVNSCOSELHEKTYLJCMGTPGHEDFVOMENEVCKLPPLSLNGV	720
Qy	700	RKFRISGTSMAKNIASTAKIENELK	744
Dp	721	RKFRISGTSMAKNIASTAKIENELK	745

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US-10-195-101-32
/ Sequence 32, Application US/10195101
/ Publication No. US20030087317A1
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Molteni, Angela
/ APPLICANT: Magnaghi, Paola
/ APPLICANT: Bobotli, Roberta
/ APPLICANT: Scaccheri, Emanuela
/ APPLICANT: Isacchi, Antonella
/ APPLICANT: Hodgson, David M.
/ TITLE OF INVENTION: HUMAN NIM1 KINASE
/ FILE REFERENCE: PC-0009-1 CIP
/ CURRENT APPLICATION NUMBER: US/10/195,101
/ CURRENT FILING DATE: 2002-07-11
/ PRIOR APPLICATION NUMBER: 09/523,849
/ PRIOR FILING DATE: 2000-03-13
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PERL Program
/ SEQ ID NO 32
/ LENGTH: 793
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: GenBank Accession No. US20030087317A1 520521888
/ DATABASE ENTRY DATE: 25 April 1997
US-10-195-101-32

```

Query Match	68.4%	Score 2555	DB 14	Length 793
Best Local Similarity	65.5%	Pred. No. 4.9e-148		
Matches 525	Conservative 82	Mismatches 105	Indels 90	Gaps 14

QY	541	ASAGSABRHOXKMSWGHPDKYTLPTIKDGSAYRPGTAORPAASPAHSISAGS--T	598
QY	505	-----TAP-----QRYVPAAPSAAHNISSGGA	526
Db	482	RKSSSAGPS--NNVYSGSGMTRRNTTYVCRSTDRVAALQNGRDSLTMSASMSGTSIV	540
QY	462	RKKTTPPSSTNSVLSTSTNRSPSLERASLQAGASLONKDS-----	504
Db	422	PSDHAGPSLPPAVSVSTTKPQANSVSEBQKEMWDQOTARLGGSTTVSGSKSEVTVPLVGPD	481
QY	408	FSDQAGPALPTNSYSKTKTOSNNAKKPEE--DESGRKASST-----AYVPAASPLGLE	461
Db	362	MATYILIGKRPFGSGSLSSGNLCQSRSSPSLNNSTLQSPHMLYQSRISANOKQRR	421
QY	355	MATYILIGKXSELG-----DTTLKPRSAULTVNSAPSEH--KVQSVSANPQRR	407
QY	295	LEQIMKDRMNVGHEDDELKPYVEPLPYKDPRTETLVMNGYTRREIQLSLVGQRYNEV	354
Db	302	LEQIMKDRMNVGHEEELKPYSEPELDLNAKRLIDIVWTGPARDLINALVQKYDEV	361
QY	242	SLGVILYTLVSSSLPFDQNLKELRERLVPRKRYVPLFMSTDENLKLVLNPLIRGS	301
QY	235	SLGVILYTLVSSSLPFDQNLKELEERLVRGKRYLPLFMSTDENLKLKFLIINPSRGT	294
Db	182	DLAENELLIDAMNLIKIDPFGSNEFTGNKLDLPFGSPPAABELEQKKYDDEVDVW	241
QY	175	DLAENELLIDAMNLIKIDPFGSNEFTGNKLDLPFGSPPAABELEQKKYDDEVDVW	233
Db	122	LFEVIEETKTLYLIMEVYASGSGVEFPLYLAHGMEKEKARAFROIVSAVOYCHQKCIYHR	181
QY	115	LFEVIEETKTLYLIMEVYASGSEVPDYLAHGRMEKEKARAFROVSAVOYCHOKFTVHR	174
QY	55	LKLTICKGNFAKVLARHILTGKEVAVKIIDKTQANSSSLQKLPREYVIMVLNHPNIYK	114
Db	62	LQTLICKGNFAKVLARHVLTRERVAVKIIDKTQANPSLQKLRERVIMKILNHPNIYK	122
QY	2	SAATPLPTLNERTTEQPLT--GHLD-----SKPSSKSMNIGRSASNSA--DEOHIGNRY	54
Db	2	SAATPLPTLNERTNHTSVDGLETTHIPKTVSSSRQNIPCRNSLTSATDEPHIGNRY	61

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QY 527 DPTNTPPGVSSRSFHFAGQLRQVDDQNNLPGVTPAPRS-----GHSGRGGAAGSIFSK 582
Db 599 PDRTFPPGSSSSRSFHFEBQL--RERSAAVSGPPAPSDTAAALAAARGSTGTGIISK 655
QY 583 PFSKVRNRNLNEPESKQDVETLRPHVVGSGNDKEKEFEPRAKPRSLRFTSMKTTSSME 642
Db 656 ITSKEVRNRDPESGASGRTDTR-----GSSEPPDKXEGKAKRSLRFTSMKTTSSMD 711
QY 643 PNEMMREIRKVLADANSCSELHEKYMLLCMHGTPEHEDFVOMEVECKLPRLSLNGVRFK 702
Db 712 PNDWREIRKVLADANTCYEQRERFLFCVHGDAQDSLQVEMEWECVCLPRLSLNGVRFK 771
QY 703 RISGTSMAFKNIASKIANELKI 724
Db 772 RISGTSIAFKNIASKIANELKI 793

RESULT 14
US-09-919-585-12
/ Sequence 12, Application US/09919585
/ Patent No. US3020115167A1
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Tian-Qiang
/ APPLICANT: Feng, Jia-Jia
/ APPLICANT: Reinhard, Christoph
/ APPLICANT: Pantl, Wendy J. T.
/ APPLICANT: Williams, Lewis T.
/ TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING PAR-1
/ TITLE OF INVENTION: POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZING
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
/ FILE REFERENCE: PP-016093.002/200130.525
/ CURRENT APPLICATION NUMBER: US/09/919,585
/ CURRENT FILING DATE: 2001-07-30
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 795
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-919-585-12

Query Match 68.3%; Score 2552; DB 9; Length 795;
Beet Local Similarity 65.2%; Pred. No. 7,5e-148;
Matches 525; Conservative 82; Mismatches 104; Indels 94; Gaps 16;

QY 3 SARPTPLPLNRDTEQPTL--GHLD----SKPSKSNMTRGNSATSQA--DEOPHIGNYR 54
Db 2 SARPTPLPVNRDTEHNTSVGYTEPHIQPKSSSRQNI PCRNSTISATDEQPHIGNYR 61
QY 55 LKKTIGKGNPKAVKLARHILGKGVAAVKIIDKTQLNSSLOKLRERVIMKVLNHPNIVK 114
Db 62 LKKTIGKGNPKAVKLARHVLGREGVAVKIIDKTQLNPTSLQKLRERVIMKVLNHPNIVK 121
QY 115 LFEVLETEKTLVLMVEYASGGEVFDYLAHGRMKEKEARAFROVAVQVCHQKFTVHR 174
Db 122 LFEVLETEKTLVLMVEYASGGEVFDYLAHGRMKEKEARAFRIIVAVQVCHQKFTVHR 181
QY 175 DLKAEKLLDADNMIKIADPGFSNEFTFGKLDTFCCSPPYAAPELFGKKYDGPEDVW 234
Db 182 DLKAEKLLDADNMIKIADPGFSNEFTFGKLDTFCCSPPYAAPELFGKKYDGPEDVW 241
QY 235 SLGVLITLVYVGSGLPFDGQNLKELRERVLRGKRIIPFYMSTDCGNLKKKFLINPSKRG 294
Db 242 SLGVLITLVYVGSGLPFDGQNLKELRERVLRGKRIIPFYMSTDCGNLKKKFLINPSKRG 301
QY 295 LEQIMKRMNVVGHEDDELKPYEPLPDYDKPRRTELNVNMGYTRREIODSLVQORYNEV 354
Db 302 LEQIMKRMNVVGHHEBELKPYTEBDDPFNTRKIDIMVTWGFAFDEINALLINQKXDEV 361
QY 355 MATVLLIGKSSSELEG-----DTITLKPRRSADLTNSAPSPSH-KVQNSVSNPQRR 407
Db 362 MATVLLIGKRPKEEGGSLSSGNLCONSRSSDLSNSTQSPHKLTVQNSISANOQRR 421

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QY	408	FSDDQGPALPRTNSNSISKTKQSNNAENKPRFE--DRESGRASST---- <td>461</td>	461
Db	422	FSDAHGPSTPPVAVSYTKRBPQANSVSEBQKEWDKVARKLGSITTVGSKSEMTASPLVGP	481
QY	462	RKKTPTPTSTNVLSVTSNTRSRNSPLLEPASLGGQASLONKQDS-----	504
Db	482	RKGSSTIPS--NNVVGSGSMARNRTVYCETTRRYVALONGKQSSLTMEVSSISAGSSV	540
QY	505	-----TAP-----	526
Db	541	ASAVPSANPRHQKSMSTSGHPFKVTLPTLKQDSBAYRPQTGRVPAPASASHSISRA--T	598
QY	527	PDRTYPPGVSRSRSTFFHAGQLRQVDDQNLPGVTTPASGSGSQ-----RKASGSIFS	581
Db	539	PDRTFFPGSSRSRSTFFHGSQI---RERSVAVNGCPASPS--HETGFAHARRCTSGIIS	654
QY	582	KFTSFVVRNLINEPESKQVETFLRPHVVGSGGNDKE--KEEPREAKRSLRPFWSMKTTS	639
Db	655	KITSFVVRNDSEGGASGRTDTSR---STSEPPERDDEBGGDSKPSRLRFTWSMKTTS	710
QY	640	SMEPENMREIRKVLVDANSQSELHEKMYLLCMHGTPGHEDPVOVOMEWEVCXLPRLSLNGV	699
Db	711	SMDPDPDMREIRKVLVDANNCDVEQERFLPLFCVHDADQDLSLVQHEMEVCXLPRLSLNGV	770
QY	700	RPKRISGTSMAPKNIASKIANELKL	724
Db	771	RPKRISGTISIAFKNIASKIANELKL	795

; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
; 25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7473244CD1
US-10-311-034-4

Query Match 68.3%; Score 2552; DB 15; Length 795;
Best Local Similarity 65.2%; Pred. No. 7.5e-148;
Matches 525; Conservative 82; Mismatches 104; Indels 94; Gaps 16;

QY 3 SARTPLPTNERDETOPTL--GHLD-----SKPSKSNMTRGRNSATSA-DEOPHIGNR 54
DB 2 SARTPLPTNERDETOPTL--GHLD-----SKPSKSNMTRGRNSATSA-DEOPHIGNR 61
QY 55 LKTIIGKNPAKYKLAHILTGKEVAVKIDKTQLNSSLQKLFREYRIMKVLNHPNIVK 114
DB 62 LQTIIGKNPAKYKLAHILTGKEVAVKIDKTQLNSSLQKLFREYRIMKVLNHPNIVK 121
QY 115 LFEVIEETKTLVYMEYASGGEVFDYVAHGRMKEKRAKFRQVVASAVQYCHQKFIYHR 174
DB 122 LFEVIEETKTLVYMEYASGGEVFDYVAHGRMKEKRAKFRQVVASAVQYCHQKFIYHR 181
QY 175 DLKAEMLLDADNNIKIADFGFNEFTFGKLDTPCGSPRYAPLFOGKYNDGPEVDW 234
DB 182 DLKAEMLLDADNNIKIADFGFNEFTFGKLDTPCGSPRYAPLFOGKYNDGPEVDW 241
QY 235 SLGVIIYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKFLILNPSKRG 294
DB 242 SLGVIIYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKFLILNPSKRG 301
QY 295 LEOIMKDRMNVGHEDELKPYVEPLDYKDPRTLEIMVSMGYTREIQQSLVQRYNEV 354
DB 302 LEOIMKDRMNVGHEDELKPYVEPLDYKDPRTLEIMVSMGYTREIQQSLVQRYNEV 361
QY 355 MATYLLGYKSSLEG-----DTITLKPRPSADLTNSAPSPH--KVQSVANPKOR 407
DB 362 MATYLLGYKSSLEG-----DTITLKPRPSADLTNSAPSPH--KVQSVANPKOR 421
QY 408 FSDQAGPALPTSNYSKKTQSNNAENKRPPE--DRESGRKAST-----AKVPASPLPGL 461
DB 422 FSDHAGPSIPPAVSYTKRPQANVESBQKEHMDVARKLGSTTVGSKSEMTASPLVGP 481
QY 462 RKTTPPTSTNSVLSTNSRNSPLIERASLGASIQNGKDS-----504
DB 482 RKSSSTIPS--NNYSGGSMARNTYCCERTDRYVALQNGKDSLTMSVSSISSAGSSV 540
QY 505 -----TAP-----ORVPVAPSAHNTSSGGA 526
DB 541 ASAVPAPRPHQKSMSTSGHPIKVTPLTIKQSGEAYRPGTKORVAPASPAHSISTA--T 598
QY 527 PDRTNPPRGVSSRSSTFHAGQLROVRDOQLPYGVTPASPSGHSQG-----RRGASGIS 581
DB 599 PDRTNPPRGVSSRSSTFHAGQLROVRDOQLPYGVTPASPSGHSQG-----RRGASGIS 654
QY 582 KPTSKFVRRLNLPESKDRVETLRPHVVGSGGNDKE--KEEFREAKPRSLRFTWSMKTTS 639
DB 655 KITSKFEVRRLNLPESKDRVETLRPHVVGSGGNDKE--KEEFREAKPRSLRFTWSMKTTS 710
QY 640 SMEPNEMREIRVVLANSQSELEHKKYMLLCHGTFPGHEDFYQWEMEVCKLPRLSLNGV 699
DB 711 SHDPNDMEIRVVLANSQSELEHKKYMLLCHGTFPGHEDFYQWEMEVCKLPRLSLNGV 770
QY 700 RFRKISGTSMAPKNIAASKIANELKL 724

DB 771 RFRKISGTSMAPKNIAASKIANELKL 795
Search completed: February 26, 2005, 18:03:59
Job time : 142 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:42:42 ; Search time 44 Seconds
(without alignments)
1583.203 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737
Sequence: 1 MSASRTPLPLTNRDEQPT.....SGTSMARKIASKIANELKL 724

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3515	94.1	745	2 G01025	serine/threonine p
2	3467	92.8	774	2 I48609	probable serine/th
3	2381	63.7	713	2 S27966	probable serine/th
4	1771.5	47.4	1192	2 T18611	probable serine/th
5	1707	45.7	1246	2 G89287	protein H39823.1 l
6	988.5	26.5	1398	2 T13741	hypothetical prote
7	981	26.3	798	2 JCT500	gk protein - chic
8	928	24.8	481	2 I49072	protein kinase - m
9	821.5	22.0	891	2 T40503	protein kinase kin
10	812.5	21.7	891	2 A38903	protein kinase 1 -
11	797.5	21.3	633	1 A26030	serine/threonine-s
12	778.5	20.8	887	2 T20941	hypothetical prote
13	776.5	20.8	651	2 S52244	p59Eg3 protein - A
14	775	20.7	602	2 S72513	FG2 protein - yea
15	757.5	20.3	512	2 T52633	serine/threonine-s
16	752.5	20.1	504	2 T07415	probable serine/th
17	745.5	19.9	512	1 JCI446	serine/threonine-s
18	744	19.9	504	2 T10449	probable serine/th
19	740	19.8	746	2 S62365	SNF1-related prote
20	727.5	19.5	511	1 A56009	serine/threonine-s
21	716.5	19.2	576	2 T41587	probable carbon ca
22	710.5	19.0	512	2 T07788	probable serine/th
23	710.5	19.0	513	1 S60303	serine/threonine-s
24	708.5	19.0	726	2 T33998	hypothetical prote
25	707.5	18.9	473	1 S59941	serine/threonine-s
26	707.5	18.9	1558	2 T29253	hypothetical prote
27	707	18.9	552	1 S51025	hydroxymethylglut
28	705.5	18.9	552	1 A53621	hydroxymethylglut
29	699	18.7	562	2 T29858	hypothetical prote

30	690.5	18.5	1016	2 T25433	hypothetical prote
31	688.5	18.4	513	1 S60304	serine/threonine-s
32	687.5	18.4	472	2 B90100	SNF-related kinase
33	687.5	18.4	510	2 T04145	serine/threonine p
34	681	18.2	1064	2 S52687	serine/threonine-s
35	679	18.2	502	1 A41361	serine/threonine-s
36	661.5	17.7	1518	2 S37928	probable purine nu
37	650.5	17.4	1147	2 S64930	serine/threonine-s
38	641.5	17.2	1142	2 S59359	G1N4 protein - yea
39	638	17.1	622	1 S44859	serine/threonine-s
40	634	17.0	915	2 S74283	probable protein k
41	633	16.9	480	2 A86427	probable serine/th
42	632.5	16.9	440	2 T14736	probable serine/th
43	624.5	16.7	489	2 T04862	probable serine/th
44	619	16.6	334	2 T22427	hypothetical prote
45	615.5	16.5	440	2 T14735	probable serine/th

ALIGNMENTS

RESULT 1

G01025
serine/threonine protein kinase - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C/Accession: G01025
R/Navarro, E.
submitted to the EMBL Data Library, April 1996
A/Reference number: H00564
A/Accession: G01025
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-745 <N>
A/Cross-references: UNIPROT:Q15524; UNIPROT:Q96H3; EMBL:X97630; NID:g1310674
F/18-271/Domain: protein kinase homology <KIN>

Query Match 94.1%; Score 3515; DB 2; Length 745;
Best Local Similarity 92.3%; Pred. No. 7.6e-125;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

QY	34	MIRGRNSATNSADROPHIGNRLLKTIGKGFAYKLAARHLTKGVAVKTIIDTQUNSSS	93
DB	1	MIRGRNSATNSADROPHIGNRLLKTIGKGFAYKLAARHLTKGVAVKTIIDTQUNSSS	60
QY	94	LQKLPFEVRIMKYNPNIVKLPFVETETKTLVLMVSYASGSEVFDLVHGMKEKEAR	153
DB	61	LQKLPFEVRIMKYNPNIVKLPFVETETKTLVLMVSYASGSEVFDLVHGMKEKEAR	120
QY	154	AKRQVSAVOYCHQKRIYHRDIAENLLIDADMNLIKIDFGFSNEPTFGNKLDTPCGSP	213
DB	121	AKRQIVSAVOYCHQKRIYHRDIAENLLIDADMNLIKIDFGFSNEPTFGNKLDTPCGSP	180
QY	214	PYAPPELFGKKKDDGPEVDWISGLVILYTVSGSLPPDQNLKELRERVLRGKRRAPFYM	273
DB	181	PYAPPELFGKKKDDGPEVDWISGLVILYTVSGSLPPDQNLKELRERVLRGKRRAPFYM	240
QY	274	STDCENLLKKFLLINPSKGTLEQIMKDRMANYGHEDDELKPYVEPLPVKXDRRTLEMY	333
DB	241	STDCENLLKKFLLINPSKGTLEQIMKDRMANYGHEDDELKPYVEPLPVKXDRRTLEMY	300
QY	334	SMGYTTEETIODSLVGORYNEVMATYLLLGKSSLEGGDTTLTKRPSADITNSAPSPSH	393
DB	301	SMGYTTEETIODSLVGORYNEVMATYLLLGKSSLEGGDTTLTKRPSADITNSAPSPSH	360
QY	394	KVGRSVSANPKORRFPDQAPALPTNSYSKKTQSNNAEKRRPEEDRESGRKASSTRAKVP	453
DB	361	KVGRSVSANPKORRFPDQAPALPTNSYSKKTQSNNAEKRRPEEDRESGRKASSTRAKVP	420
QY	454	ASPLPGLERKKTPTPTSTNSVLSTSTNRSHNSPLLRASIGQASIONGXK-----	503
DB	421	ASPLPGLERKKTPTPTSTNSVLSTSTNRSHNSPLLRASIGQASIONGXKSLTMPGRAS	480

QY 504 -----STAPORVPVAPSAHN 519
DB 481 TASASAGVSAARPROHOKSMGSHVHPNKASGLPTESNCEVPBPSTAPORVPVAPSAHN 540
QY 520 ISSSGAPADRTNPRGVSSRSTFPAAGOLROYRDOONLPGVTPASPSPAGSGGRGASGSI 579
DB 541 ISSSGAPADRTNPRGVSSRSTFPAAGOLROYRDOONLPGVTPASPSPAGSGGRGASGSI 600
QY 580 PSKTSKFRVRNLPESKDRVETLRPHVVGSGNDKEKEFRBAKPRSLRFTWSMKTTS 639
DB 601 PSKTSKFRVRNLPESKDRVETLRPHVVGSGNDKEKEFRBAKPRSLRFTWSMKTTS 660
QY 640 SMEENEMREIRKLDANSOSSEIHEKXMLCMHGTGCHDFVQWEMEVCPLRLSLANGV 699
DB 661 SMEENEMREIRKLDANSOSSEIHEKXMLCMHGTGCHDFVQWEMEVCPLRLSLANGV 720
QY 700 RFKRISGTSMAFKNIAKIANELKL 724
DB 721 RFKRISGTSMAFKNIAKIANELKL 745

RESULT 2

148609
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C/Accession: I48609; S31333
R/Inglis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A/Title: Emk, a protein kinase with homology in yeast maps to mouse chromosome 19.
A/Reference number: I48609; MUID:93364122; PMID:8358177
A/Accession: I48609
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-774 <ING1>
A/Cross-references: UNIPROT:Q05512; EMBL:X70764; NID:G57919; PIDN:CAAS0040.1; PID:G57920
R/Inglis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A/Description: A novel protein kinase with homologues in yeast maps to mouse chromosome
A/Reference number: S31333
A/Molecule type: mRNA
A/Residues: 1-698; 'K', 700-702, 'GRGLPTAAKASCTSGTCYCAHQAHTRR', 731-774 <ING2>
A/Cross-references: EMBL:X70764
C/Genetics:
A/Gene: emk
C/Superfamily: protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F/51-304/Domain: protein kinase homology <KIN>
F/59-67/Region: protein kinase ATP-binding motif

Query Match 92.8%; Score 3467; DB 2; Length 774;
Best Local Similarity 88.3%; Pred. No. 4.9e-123;
Matches 687; Conservative 11; Mismatches 22; Indels 58; Gaps 3;

QY 1 MSARTPLPTINRDPEOPTLGHLDSPSSKSMNIRGMSATSADOPHIGNVRLIKTIG 60
DB 1 MSARPLPTINRDPEOPTLGHLDSPSSKSMNIRGMSATSADOPHIGNVRLIKTIG 60
QY 61 KGNFAVKLARHILITGKEVAVKIIDKTQNLSSLOKLFREVRIMKVLNPNIVKLFVIE 120
DB 61 KGNFAVKLARHILITGKEVAVKIIDKTQNLSSLOKLFREVRIMKVLNPNIVKLFVIE 120
QY 121 TEKTLVLMVEYASGGEVDYLVAHGMRKEKARAKRQVSAVOYCHQKFIYHRDLKAE 180
DB 121 TEKTLVLMVEYASGGEVDYLVAHGMRKEKARAKRQVSAVOYCHQKFIYHRDLKAE 180
QY 181 LLLDADNMIKIADFGSNEFTFGNKLDTFGSPPYAAPLFOGKKYDGEVDVWSLIG 240
DB 181 LLLDADNMIKIADFGSNEFTFGNKLDTFGSPPYAAPLFOGKKYDGEVDVWSLIG 240
QY 241 YTLVSGSLPFDGONKELREVRILRGKRYIPFYWSTDCEMLKKFLILNPSKRGTLLEQIMK 300

DB 241 YTLVSGSLPFDGONKELREVRILRGKRYIPFYWSTDCEMLKKFLILNPSKRGTLLEQIMK 300
QY 301 DRMMNVGHEDDLKPYVEPLPYDKPRTELMVWSMGTYEEIIDSILVGORVNEVATYLL 360
DB 301 DRMMNVGHEDDLKPYVEPLPYDKPRTELMVWSMGTYEEIIDSILVGORVNEVATYLL 358
QY 361 LGYKSELLEGDTITLKPESADLTNSAPSPSHKVQSVSANPKQRRPSDQGAIPISN 420
DB 359 LGYKSELLEGDTITLKPESADLTNSAPSPSHKVQSVSANPKQRRPSDQGAIPISN 418
QY 421 SYSKTQSNANNAKKEPEERRESGRKASAKVAPLPLGLEKKTTPPTSTVSLSTGN 480
DB 419 SYSKTQSNANNAKKEPEERRESGRKASAKVAPLPLGLEKKTTPPTSTVSLSTGN 476
QY 481 RSRNSPLERASLQASLQNGKD----- 503
DB 477 RSRNSPLERASLQASLQNGKD----- 503
QY 504 -----STAPORVPVAPSAHNISGAGADRTNPRGVSSRSTFHAQ 546
DB 537 KASGLPTESNCEVPBPSTAPORVPVAPSAHNISGAGADRTNPRGVSSRSTFHAQ 596
QY 547 LRQVRDOONLPGVTPASPSPAGSGGRGASGSIKFTSKFVRNLPESKDRVETLRP 606
DB 597 LRQVRDOONLPGVTPASPSPAGSGGRGASGSIKFTSKFVRNLPESKDRVETLRP 656
QY 607 HVVVGSGNDKEKEFRBAKPRSLRFTWSMKTTSMEENEMREIRKVDANSOSSEIHEK 666
DB 657 HVVVGSGNDKEKEFRBAKPRSLRFTWSMKTTSMEENEMREIRKVDANSOSSEIHEK 716
QY 667 YMLLCVHGTGCHDFVQWEMEVCPLRLSLANGVPRKRIISGTSMAFKNIAKIANELKL 724
DB 717 YMLLCVHGTGCHDFVQWEMEVCPLRLSLANGVPRKRIISGTSMAFKNIAKIANELKL 774

RESULT 3

S27966
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - human
N/Alternate names: protein p78
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C/Accession: S27966
R/Maheshwari, K.K.; Som, S.; Parsa, I.
submitted to the EMBL Data Library, January 1992
A/Description: Sequence of a cDNA encoding 78kD marker protein lost in chemically induce
A/Reference number: S27966
A/Accession: S27966
A/Molecule type: mRNA
A/Residues: 1-713 <MAH>
A/Cross-references: UNIPROT:P27448; EMBL:M80359; NID:G189511; PIDN:AAAS9991.1; PID:G1895
C/Superfamily: protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F/54-307/Domain: protein kinase homology <KIN>
F/62-70/Region: protein kinase ATP-binding motif

Query Match 63.7%; Score 2381; DB 2; Length 713;
Best Local Similarity 66.2%; Pred. No. 1.8e-82;
Matches 498; Conservative 75; Mismatches 109; Indels 70; Gaps 18;

QY 3 SARPLPTINRDPEOPTLGHLDSPSSKSMNIRGMSATSADOPHIGNVRLIKTIG 57
DB 2 STRPLPTINRDPEOPTLGHLDSPSSKSMNIRGMSATSADOPHIGNVRLIKTIG 60
QY 58 TIGKGNFAVKLARHILITGKEVAVKIIDKTQNLSSLOKLFREVRIMKVLNPNIVKLF 117
DB 61 TIGKGNFAVKLARHILITGKEVAVKIIDKTQNLSSLOKLFREVRIMKVLNPNIVKLF 120
QY 118 VIEFEKTLVLMVEYASGGEVDYLVAHGMRKEKARAKRQVSAVOYCHQKFIYHRDLK 177
DB 121 VIEFEKTLVLMVEYASGGEVDYLVAHGMRKEKARAKRQVSAVOYCHQKFIYHRDLK 180
QY 178 AENLLDADNMIKIADFGSNEFTFGNKLDTFGSPPYAAPLFOGKKYDGEVDVWSLIG 237

181 AENLLADADNMKIKADFGSNEPFTVGKLDITFCGSPFYAAPELFQGGKTYGPEVDWISLG 240
QY 238 VIITVTVSGSLPFDGQNLKELREYVLAGKTRIPFYMSTDCBNLKKTLINPSKRGTLQ 297
Db 241 VIITVTVSGSLPFDGQNLKELREYVLAGKTRIPFYMSTDCBNLKKTLINPSKRGTLQ 300
QY 298 IMKDRMNVGHDEDELKPYVEPLPDYDPRRTLMVMGMGTREIIOSLVGQRNEMMAT 357
Db 301 IMKDRMNVGHDEDELKPYVEPLPDYDPRRTLMVMGMGTREIIOSLVGQRNEMMAT 360
QY 358 YLLLVKSELEGGDTITLKRPSPADLTNNSAPSPSHKQSVSANPQRRFSDQAGPAIP 417
Db 361 YLLLVKSELEGGDTITLKRPSPADLTNNSAPSPSHKQSVSANPQRRFSDQAGPAIP 411
QY 418 TNSYSYKKTQSNNANENKRPEDRESGRKASSTAK---VPASPLPG-----LER 462
Db 412 SYVAAPKRSQSTVSADSL-KEDGISRKSSTGSAVGKGIAPASPMGLNAGNPNKADIPER 470
QY 463 KKTTPPSTNSVLTSTNSRSPSLERASLGAS-1ONGKD-STAP-QRPVPAPEAHN 519
Db 471 KKSSTVPSSTNTPAGGCMTRRN-TYVCSERTTDDRHSVIONGENSTLPDQRTVA--STHS 527
QY 520 ISSSGAPDRTPNPRGVSSRSTFHAQOLRQVDOQNLPGVTPASPS-GH-----SQGR 573
Db 528 ISSA-ATPDRIRPRPGTASSTFHG---QPRERTATYNGPRAPSPSLSHSATPLSGTRS 562
QY 574 GAGSSTFSKFTSKFVR-RNINPEBSKQDVETLAPHVVGSGANDKEKEEPKAPRSIRFT 632
Db 583 RGSSTVPSKLTSLKTRSRNVSA-----KQKQENKEAKPRRSIRFT 621
QY 633 WSKHTTSSMEPNEMREIRRYVLNANSGOSELHEKMYLLCMHGTPGHEDPFQWEMEVCKLP 632
Db 622 WSKHTTSSMEPNEMREIRRYVLNANSGOSELHEKMYLLCMHGTPGHEDPFQWEMEVCKLP 661
QY 693 RLTLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db 682 RLTLNGVRFKRISGTSMAFKNIASKIANELKL 713

RESULT 4
T18611
probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18611; T23144; T23143
R/McMurray, A.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z18997
A/Accession: T18611
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1192 <M11>
A/Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; P1DN:CAB54179.1; GSPDB:GN00023; CESP:H39E23
A/Experimental source: clone AH10
A/Accession: T18610
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-487,536-1192 <M12>
A/Cross-references: EMBL:Z81027; P1DN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b
A/Experimental source: clone AH10
R/McMurray, A.
submitted to the EMBL Data Library, June 1997
A/Reference number: Z19696
A/Accession: T23144
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1192 <M13>
A/Cross-references: EMBL:Z26102; P1DN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
A/Experimental source: clone H39E23
A/Accession: T23143
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-487,536-1192 <M14>
A/Cross-references: EMBL:Z26102; P1DN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b
A/Experimental source: clone H39E23
C/Genetics:
A/Gene: CESP:H39E23.1a; CESP:H39E23.1b
A/Map position: 5
A/Intons: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 99
C/Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pr
F/1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #
F/1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short spli

Query Match 47.4%; Score 177.5; DB 2; Length 1192;
Best local Similarity 39.0%; Pred. No. 1.8e-59;
Matches 423; Conservative 106; Mismatches 179; Indels 377; Gaps 25;

QY 2 SSARPTPLNERDTEOPLTGLHDS--KSSKSNMIRGNATSADQPIGNRYLLKTI 59
Db 123 SSAR-----YSSGSRHPTSGSSSHARSIGSGM--SSRGAARNDDQVHVGVKYLKTI 176
QY 60 GKGNFAKVKLARIILKGYAVVNIIDKQLNSSLQKLPREVIMVNLNPNVYKPEVI 119
Db 177 GKGNFAKVKLAKVITGHEVAIKIIDKTLNPSLQKLPREVIMVNLNPNVYKQVM 236
QY 120 ETEKTLVLMVEYASGGEVFDYLAHGRMKEKARAKFRQVSAVOYCHQKFIYHRLKAE 179
Db 237 ETEQTLVLEVASGGEVFDYLAHGRMKEKARAKFRQVSAVOYHLSNIIHRLKAE 236
QY 180 NLLLDADNMKIKIADFGSNEPFTGKLDITFCGSPFYAAPELFQGGKTYGPEVDWISLGI 239
Db 297 NLLLDADNMKIKIADFGSNTFTSLGNKLDITFCGSPFYAAPELFQGGKTYGPEVDWISLGI 356
QY 240 LYTVSGSLPFDGQNLKELREYVLAGKTRIPFYMSTDCBNLKKTLINPSKRGTLQ 299
Db 357 LYTVSGSLPFDGQNLKELREYVLAGKTRIPFYMSTDCBNLKKTLINPSKRGTLQ 416
QY 300 KDRMNVGHDEDELKPYVEPLPDYDPRRTLMVMGMGTREIIOSLVGQRNEMMAT 356
Db 417 KDRMNVGHDEDELKPYVEPLPDYDPRRTLMVMGMGTREIIOSLVGQRNEMMAT 476
QY 357 TYLLLVKSELEGGDTITLKRPSPADLTNNSAPSPSHKQSVSANPQRRFSDQAGPAIP 417
Db 477 TYLLLVKSELEGGDTITLKRPSPADLTNNSAPSPSHKQSVSANPQRRFSDQAGPAIP 536
QY 377 ---PRPSADIT-----NSAPPS----- 330
Db 537 SRYSRSSATATGASITAGSALASANAOKHQSSAPSSGSSSSRRSQNDAAATAGCT 536
QY 391 ---PSHKVQRSSVS----- 400
Db 597 VVNSGTRHGGVQNRAPTSRQATISLLQPSYKPSNTTQIAQIPPLFNENSTATSSAQ 656
QY 401 ---ANPK-----ORRFSDQ--- 411
Db 657 PSYGTIGTRKIKADPKRIRPLNSTAVGQHGHTATGAVANNGGISHRDHAGQOQVNLGTS 716
QY 412 ---AGPALPTNSYSKKTQS-----NNAS 432
Db 717 STWMSKILNKTPAAGTAAATSSSSSSATSTABLQKSGQISHAPTEPVREDDEENSE 776
QY 433 NKR-----PEERDEG-----RKASSAPKYPASPLPLGERKKT 466
Db 777 NQNGNVPLIGVGVPQTSFAVOVTEBATSSDKQOQKASS--ETPKSKPSMIIHSPS 834
QY 467 PTPS-----TNS-----V 474
Db 835 MPSPQMMTAMESLKLSESGGTGSPVATGGPPQATSGQMSRATNTNSAMGASSGGAA 894
QY 475 LSTSTSRKNSPLLEPASLGQASIQ-----NGKSTAPQV 510
Db 895 PASATQNLGAP---SSTGASQOQYHPRAPSSSSSSSTNPRHQQLTHNAPSPVTPSSY 950
QY 511 PVASPSAHNIISSG--GAPDRTPFRGVSSRSSTFHAQOLRQV--DQQNLPGVTPASPS 566

Db 951 QIPSTAVNTVSTGMPSSSSSAFPRNTRKQTH-GKTEKDKGDDSSPEIGETPGNVS 1009
QY 567 GHSOG--RRGASGSIFFSKTFSKYRNLNBPESKDRVETLLRPHVVSGGNDKEKEFR-- 622
Db 1010 IGATGPSANNAEATYWSKL-SKLTRRDHNR-ESWTCQVSGAGCTIGASQCGQTAALAI 1067
QY 623 -----EAKRSLRFTWMSMTTSSMENEEMREIRKYLDA NSC 659
Db 1068 REOSGPIAPGAGVAPSLPIHESGVKPRSLRFTWMSMTTSSLAVDMMREIRKYLDA NSC 1127
QY 660 QSEIHEKMYLNCMHGTGHEDEVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIA 719
Db 1128 DYERREKRYMLCTVGDNDTSLVQWEMEVCKLPRLSLNGVRFKRISGTSIGFKNIASKIA 1187
QY 720 NELKL 724
Db 1188 QELNLT 1192

RESULT 5

G89287
Protein H39E23.1 (imported) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: G89287
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see webstiles genome.wustl.edu/gen/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: G89987
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1246 <STO>
A/Cross-references: GB:chr_V; PIDN:CAH09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.
C/Genetics:
A/Gene: H39E23.1
A/Map position: 5

Query Match 45.7%; Score 1707; DB 2; Length 1246;
Best Local Similarity 34.1%; Pred. No. 5e-57;
Matches 420; Conservative 113; Mismatches 174; Indels 524; Gaps 24;
QY 15 DTBQPTLGHLDSPSSKSMIRGNATSA---DEOPHIGNYLLTKIGKNFAKYKLAR 71
Db 19 DGDVTHNRKSSSHASTGQSGMSSRSARNDQVHVGKYLTKTIGKNFAKYKLAK 78
QY 72 HLTGKEVAVKIIDKTQNLNSSLQKLFREVRIMKVLNHPNIVKLFEVIEETKTYLWMEY 131
Db 79 HVTGHEVAIKIIDKTALNPSLQKLFREVKIMKQDHPNIVKLYQVMEBQLYLVLEK 138
QY 132 ASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYCHOKPTVHRDLKAENLLDADANNIKI 191
Db 139 ASGGEVFDYLVAHGRMKEKARAKFRQVSAVOYLSKNIIHRDLKAENLLDADANNIKI 198
QY 192 ADGFGNEFTFGMKLDTFGCSPRYAAPLFGKKYGPEDVWSLGVILYTLVSGSLPDP 251
Db 199 ADGFGNFTSLGKMLDTFGCSPRYAAPLFGSGKYGPEDVWSLGVILYTLVSGSLPDP 258
QY 252 GQNLKELRERVLNGKTRIPFYMSSTDENILKKEFLINPSKRGLEQIMDKRMNVGHEDD 311
Db 259 GQNLKELRERVLNGKTRIPFYMSSTDENILKKEFLINPSKRGLEQIMDKRMNVGHEDD 318
QY 312 ELKPYVEPLPDYKDPRTBLMV--SMGYTRBIIODSLVQRYNEWATYLLGYKSESL 368
Db 319 ELKPYFEPDPQDDEQRIEKLQIFQGFYKAILSEVEKEKEDIHATYLLGKESKM 378
QY 369 EGGTITLK-----PPSADLT- 384
Db 379 DASEITMAOSLSHSSINVSLSGHPAGVITREHTSSASGSSASPSRYSRSSATATG 438

QY 385 -----NSSAPB----- 390
Db 439 ASITGASALASANAANKHQSSAAPSGBSSSSRSSQNDAAATTAAGTVMSGTRHGVQ 498
QY 391 -----PSHKVQRSVS-----A 401
Db 499 MRAQPTSRQATISLQPPSKSSNTQTQIAQIPLFNRRNSTSSAAQPSGTGTGRKIA 558
QY 402 NPK-----QRPSDQ----- 411
Db 559 DEKGRIPILNSTAVOGHRTATGAVAANNNGIPSHRDHAQQQYWMQLTSSTWMSKLINKTP 618
QY 412 -AGPALPSSNSYKKTQS-----NNAEKR----- 435
Db 619 AAGGTAAVSSSSSSATSTAPLQKSGQISHAPEPVIREDDENNENGNVPLIGGV 678
QY 436 -----PEDESG-----RKASSTAKVPASP- 457
Db 679 GPOTSPAVGVPTEDATSSSDKXQQQKASSETPKESNPIVMQNLNLNLSKSLDSSAAT 738
QY 458 -----PELRKKTPT----- 468
Db 739 SYETPRRPGIAGRSEPSATPRRRHQTVVVDARHLQTPDTPRPHEDTTLDRQML 798
QY 469 -----PSINSVLS-----TSNRRSN-----SPLER 490
Db 799 YVSTASRMTGVLPTPTSNSTSSFIYEPILTHVAASPDITTTPTKSVTTSYPFR 858
QY 491 ----- 490
Db 859 TPSFPMVLIVLLCDNGLRPMSTMHQSPMPSQMTAMBSLKLSGSGQTGPTVATGG 918
QY 491 -----ASLGQAS----- 497
Db 919 PPORATSQQMSRATNTASNGASGGAAMASATNOLSGAPSSYGASSQOYHPAPSS 978
QY 498 -----IQNGKDSAPQVRVPAAPSAHHSSSG--GAPDRNTPRGVSRSTP 542
Db 979 SSSSTNPHQOLTHNASFSTPSYQIPTSTAVNTSTGPTSSSSAFAFRNTRKQTF 1038
QY 543 HAGQLRQVR--DOQNLPGVTPASPSPGSGG--RRGASGISFKSTKFXVRNLNBPESK 598
Db 1039 H-GKTEKXGDDSDDEIGETPGNVSIGATGPSANNAEATYWSKL-SKLTRRDHNR-ESM 1095
QY 599 DREVTLRPHVVSGGNDKEKEFR-----EAKRSLRFTW 633
Db 1096 TQPVSGRAGTIGASQCGQTAALAIAPRQSGPIAPGAGVAPSLPIHESGVKPRSLRFTW 1155
QY 634 SKKTSMEPNEMMEIRKVLDA NSCQSEIHEKMYLNCMHGTGHEDEVQWEMEVCKLPR 693
Db 1156 SKKTTSSLA PDMMEIRKVLDA NSCQDYEQREKRYMLCTVGDNDTSLVQWEMEVCKLPR 1215
QY 694 LSLNGVRFKRISGTSMAFKNIASKIANELKL 724
Db 1216 LSLNGVRFKRISGTSIGFKNIASKIAQELNLT 1246

RESULT 6
T13741
hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: T13741
R:Murphy, L.; Harris, D.; Barrell, B.
Submitted to the EMBL Data Library, April 1999
A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A/Reference number: Z17668
A/Accession: T13741
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1398 <MOR>
A/Cross-references: UNIPROT:O77268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA2
C/Genetics:

A/Cross-reference: FlyBase:FBgn000667
A/Introm: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A/Note: EG:22E5.8

Query Match 26.5%; Score 988.5; DB 2; Length 1398;
Best Local Similarity 35.1%; Pred. No. 4.1e-30;
Matches 266; Conservative 99; Mismatches 230; Indels 163; Gaps 20;

```
QY PSSKSNMIRGRNATSD-----EQPHIGNYRLKTKGKGFAYVKLARHILTGKEVAVK 82
DB 112 PSEPTSSAV-GAGGISGDKLKLKPMRVGVFDIERTTGKGFVAVVKLARHRTTKNEVAIK 170
QY 83 IIDKTQLNSSLQKLFREVRIMKVLNPNIVKLFVETETKTYLVMEYASGGEVPDYLV 142
DB 171 IIDSGQDQNTNLOKVVREVEIMKRLKPHIILKYQWETKMTIYVEYASGGEIFLYIA 230
QY 143 AHGMEKEKAPKFRQVAVQYCHQKFIYHRDIKAENLLLDADMTIKIADFGFSNEFTF 202
DB 231 KYGMSBSARFKFWQIISAVEYCHKKGIYHRDLKAENLLLDADMTIKIADFGFSNFKP 290
QY 203 GNLDTFCGSPRYAPRELFOGKATDGPEDVWVSLGVILTYLVSGSLFPDQNLKELREY 262
DB 291 GBLATWCGSPRYAAPRELFOGKATDGPEDVWVSLGVILTYLVSGSLFPDQNLKELREY 350
QY 263 LRQKRIPIFYMSTDCENILKKFLILNPSKRGTELOIMKDRM-----NYGHE 309
DB 351 LGGRFRPIFYMSSCEHLIRMLVLEPTRTTIDQIGHRMCELEHVLAKYNG-- 408
QY 310 DBELKPYEPLPDYKDRTELWVS-MGYTREELQDSLVGQRYNEVATYLLLGYSSEL 368
DB 409 -AERQTSVEPSEDI-----LRIMAEYVIGSDKTRASLKKNTYDHAIVYLL----- 455
QY 369 EDQITIKRPSADLNTS---SAPSPHKQKQSVSANPKORRPSDQGRALPTNSYSK 425
DB 456 -QDRVSHKKEQSGLSALASSTSSASRMITYSSNDQPTQOOSQOOSKTISTSIAXD 514
QY 426 TQSNNAENKRPREDRESGRKASSTAKYPAAPLPGLERK----- 463
DB 515 QCHKRLSRHQTVMSEKNAHAGATPTVP-DPGEPYAKYGPLOLPPLTGHSHLTGYLNG 573
QY 464 -----KTPPTSTNSVLSTSTNR---SNPSLLEBASLGQASIQ 499
DB 574 GGYEVDSAGIPLPMRYTPLPPTAASPAPNSCSTSSRGHSLSSSPSRHRYALISLID 633
QY 500 N-----GKSDTAQORVPVAPSAHNISSGCAPDRNTYPPGVSSRGTFA 544
DB 634 NNPSLANLRCREMKEMAGGPGVAGVPLASKOLHQTISEFLIKQSTEDCALLLQOSTAVA 693
QY 545 -GOLRQVRDQONTL---PYGVTPASPS-----GHSGRAGASGIFSKPTSKF 587
DB 694 EGKDDPKKASSVGGVPPASTTPTSTTAQPSGSAPCPGEINKTKITWSSSSSPFSK- 752
QY 588 VRBNLNE-----PESKDRVETL-----RPHV---VSGGNDKEKEFEREA 624
DB 753 --ANLQGSFRYKMSAEKSLFQTLQESPLPVEQRTKRVHVGSTNGSGD----- 800
QY 625 KPRSLRFTSMKTTSSMEPVEMKREIRKVIDANSQSGE 662
DB 801 -----SGOETNDAKSNGDSRSEKVVLAQSSSTD 829
```

RESULT 7

JC7500
qik protein - chicken
N/Alternate names: Qln-induced kinase
C/Species: Gallus gallus (chicken)
C/Date: 17-Nov-2000 #sequence_rev1510 17-Nov-2000 #text_change 09-Jul-2004
C/Accession: JC7500
R/Xia, Y., Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A/Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
A/Reference number: JC7500
A/Contents: Embryo fibroblasts

A/Accession: JC7500
A/Molecule type: mRNA
A/Residues: 1-798 <XIA>
A/Cross-reference: UNIPROT:Q91A88; GB:AF219232
C/Comment: This protein, a member of the AMPK/SNFI family of serine/threonine kinases,
C/Genetics:
A/Genes: qik
C/Keywords: protein kinase

Query Match 26.3%; Score 981; DB 2; Length 798;
Best Local Similarity 34.4%; Pred. No. 4.5e-30;
Matches 250; Conservative 106; Mismatches 201; Indels 170; Gaps 19;

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QY 42 TSADQEP-HIGNYRLKTKGKGFAYVKLARHILTGKEVAVKIIDKTQLNSSLQKLFRE 100
DB 14 SAAQPRLRVGFVDIERTTGKGFVAVVKLARHRTTKNEVAIKIIDKTQLNSSLQKLFRE 73
QY 101 VRIKVLNHPNIVKLFVETETKTYLVMEYASGGEVPDYLVAHGMEKEKAPKFRQV 160
DB 74 VOIMKLNHPHIIKLYQWETKMTIYVEYASGGEVPDYLVAFKMGEMFDHLTNGHLSSEAKKFWQIL 133
QY 161 SAVQYCHQKFIYHRDIKAENLLLDADMTIKIADFGFSNEFTFGNKLDTFCGSPRYAPREL 220
DB 134 SAVEYCHSHIIVHRDLKTEVLLDADMTIKIADFGFNFGYKSGEPLSTWCGSPRYAPREL 193
QY 221 FOGKATDGPEDVWVSLGVILTYLVSGSLFPDQNLKELREYLRVLRGKRIPIFYMSTDCENL 280
DB 194 FEGKEYEGPHLDIWSLGVILTYLVCGSLFPDQNLPLLRQVLEGRFRPIFYMSEDETL 253
QY 281 LRKFLILNPSKRGTELOIMKDRMNYGHEDELPK-----YVEPLPDYKDRPTE 330
DB 254 IRMLVVDPRKRTTIQIKQHKMNA---DPSLRQOOSLSFSQONTNSLGDITNE-QVLG 309
QY 331 LMTSMGYTREELQDSLVGQRYNEVATYLL-----GYSSSELEGDTT---LKPRPSAD 362
DB 310 IMQTLGIDRQRTVESLQNSYNHFAIYVLLERLKEYSRQSSRPATRGQGRPR-SSS 368
QY 363 LMTSSAP-----SPSHKQKQSVSA-----NPKORRPSDQGRALPTS 419
DB 369 ISNAEMPQDSLTSRSLLYQOPQSLQPSLQAEKDCMNNPLQVFPF---PVDPNF 424
QY 420 N-----SYSKTQSNNAENKRPREDRESGRKA-----SSTAK----- 451
DB 425 NGLPFRKRSISPSLLETTISEVROKELDEIKAYDHPRIKISNTSRRTTAEVTTHTF 464
QY 452 -----VPASPLPG-----LERKKTPTPTSTNSVLSTSTN 480
DB 485 QHAPCIVISSASPTGRTSSDCLTSSNSDSVALSSCLAGQVMTGSPATAMTSAFLA 544
QY 481 RSNNSPLLE-----RASLGQASIQNGK---DSTAQORVPV----- 512
DB 545 SOSDAPVLQVQCMGASLLPVSFQGRASDSTLQGKAQFRQOLRKARAKFLGLANK 604
QY 513 -----ASPSAHNISSGGAPDRTPPPGVSSRS---TFH 543
DB 605 IKGFAPQVCOSSSSRAASAMSPFGHAPFTTCYSSSGSSRBERNLLEETLQQRNLQLO 664
QY 544 AGOLRQVRDQONTLPYGVTPASPSGHSQGRGASGIFSKPTSKFVRNINLBPESKORVET 603
DB 665 HHQLQRPACPDQTSQTSATNGLPSPSDAGTCXKANSNL---LTSLEQENSHLAFGNSQL 721
QY 604 LRPHVTVG 610
DB 722 LQHPFPG 728
```

RESULT 8

I49072
protein kinase - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_rev1510 02-Jul-1996 #text_change 16-Aug-2004
C/Accession: I49072
R/Ruitz, J.C.; Conlon, F.L.; Robertson, E.J.

Mech Dev. 48, 153-164, 1994
 A:Title: Identification of novel protein kinases expressed in the myocardium of the deve
 A:Reference number: 149071; MUID:95200798; PMID:7893599
 A:Accession: 149072
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-481 <RES>
 A:Cross-references: EMBL:U11494; NID:G959420; PIDN:AAA67926.1; PID:G959421
 C:Superfamily: protein kinase homology
 C:Keywords: ATP
 F:71-324/Domain: protein kinase ATP-binding motif
 F:79-87/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 928; DB 2; Length 481;
 Best Local Similarity 48.2%; Pred. No. 2,6e-28;
 Matches 186; Conservative 75; Mismatches 97; Indels 28; Gaps 7;

QY 40 SATSADROP-HIGYVRLLKTIKGKGFARVKAARHLLTGKGVAVKIIIDQTQLSSLOKLF 98
 DB 59 SGGRSGOKPLRGVGYDVERTLGGKGFVAVKRGHNVYTKTQVAKIKIDKTRLDSSNLEKTY 118
 QY 99 REVRIMKVLNHPNIVKLFVETETKTYLVMEYASGGEVFDLVAGHMKKEARAFKQ 158
 DB 119 REVQVLMKLNHPNIIKLYQVWETKMLYIVFPAKNGEMFDVLTSGHLSNEHARQKFKQ 178
 QY 159 VSAVOYCHQKTYIHRDIAKENVLLIDAMNLIKADFGFSNEFTFGNKLDFTGSPPYAP 218
 DB 179 ILTAVYECNNHHIYHRDLKTENLLDSSNMIDIKLADFGCFGFYKPEPPLSTCVGSPPYAP 238
 QY 219 ELFGKKYDDEPVVWVSLGYLVLYVSGSLFPDGNLKEIARVLRGKRIFFVNSTDE 278
 DB 239 EVEGGEKYEABQDLVWVSLGVLLVYVCGSLFPDGNLFTLRQVLEGRFRIFPMSODE 298
 QY 279 NLKKFLLPLPSKRGTELOIKMDRMNVG---HEDD--ELKPYEPLPDYKDPRTETL 331
 DB 299 TLIRMLVYDPAKRITITAOIRQHNMQADPLLQDDPAFPMQGTSTNLGDYNE-QVLCI 357
 QY 332 MWSMGTRBEIIQDSVGQRVNEVMATYLLGKSSLELGDITTLKPRPADLTNSSAPSP 391
 DB 358 MQLALIDRQRTISLQSSVYHFAIYYLL-----LE-----RLKEHRSAGPSSRPPTAP 407
 QY 392 SHKVGKSVSANPKQRRFSDQAGPAIP 417
 DB 408 TRQ-----PQLRSSDLSLEVP 424

RESULT 9
 T40503
 protein kinase kint - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
 C:Accession: T40503
 R:Gwilliam, R.; Rajindram, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL data library, September 1998
 A:Reference number: Z21933
 A:Accession: T40503
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-891 <GMT>
 A:Cross-references: UNIPROT:P22987; EMBL:AL011534; PIDN:CAA20726.1; GSPDB:GNO0067; SPDB:
 A:Experimental source: strain 972h-, cosmid c4f6
 C:Gene: SPDB:SPBC4f6.06
 C:Map position: 2
 C:Superfamily: protein kinase homology

QY Query Match 22.0%; Score 821.5; DB 2; Length 891;
 Best Local Similarity 28.4%; Pred. No. 4.6e-24;
 Matches 241; Conservative 121; Mismatches 319; Indels 169; Gaps 24;

QY 3 SARTPLPTINERTEO-----PTLGHLDSPKSKNMIRGRSATSADQPH-----TGY 53
 DB 83 SSRKPLPASPSTRDGLRVVSGH-----SYSDKPRPRRKVIGNY 125

QY 54 ILKLTIGTNGNFAKVTALRHIIITGKEVAKKI-----DKTQLNSSSLQKL 97
Db 126 VLKRTIGAGSGMGAHVAAHLKGTGEQFAIKITVRLHPDITTKAKAAASAATYAAQSEKNKE 185
QY 98 FREVA---IMKVLNPNIVKLFEVLETEKTYLVMEVAGEVDFDYLVAAHGRMEKEARA 154
Db 166 IRTVAEALSTLIRHPYICEARDDVYITNSHYYVFEFVDGQMDIYIISHQKLKQKARK 245
QY 155 KFRQVVAHVQCHQKTYHBDLKAENLLDDAMNIKIADPGFSNEFTFGKLDTPCGSP 214
Db 246 FVRQGSALSYLHQNSVVRHDKLTENILISKTGCIKIIDFGLSNLYRQSRSLRTFCGLY 305
QY 215 YAAPLFGCKYVDGEVDMVMSLGYLVLYTVGSLPFGQNLKELREVLREKRIIPFMS 274
Db 306 FAAPFLMAQPYITGEVDMVMSFGVLYLVYVCGKPPDDQNSALHAKIKGTVEYPSLS 365
QY 275 TDCENILKKFLILNPSKKGTEQIMKORMMNVGHED-----DELKPYEPLPYDKPRR 328
Db 366 SDCKGLSRMLVTPLKXATLEVLNHPWMLRNEGPAPAPRSPITLPL-----DPEI 421
QY 329 TELMWSMY-----TRETIQSLVQGRYNEWMAVLYLLIGYSSLEGGDTITLKRPSA-D 382
Db 422 IRENNQDFGPEPKIVRELTYVISSEAYQSLAKTGFYSGPNSADKKSFEBFRIRHAMD 481
QY 383 LTNSGAPSPSHVQORSVANP-----KORRPSDAG-----PAIPTSNSYAKT 426
Db 482 IENPLPLSMWMTDYDAFHLIISTYIVSRRYEKGGMNRIAKTPVSSVESPVOPT 541
QY 427 QSNNAENKRP-----BDRESGRASSTAKVPASPLGLEBKTTPTPTNSVLST---- 477
Db 542 SYNRLTPMPPEVNAVYKGBESFRVSRNTSLARRKPLDTE--SHSPSPATSSIKKNPS 599
QY 478 -----STTKRNSPLERASLGQASIQNGKDSAPQVPAVSAHNISSSGAPDPTNF 532
Db 600 IFRFPSSRRKKNKSTSTLQI-SAPLETQSPPPTPKPSHKRP--VSYKNKLVTQSAI 655
QY 533 PRGVSSBSTFAAGOLARQV-----RDOQNLPLYGV---TPASPGSHQGRRASG 577
Db 656 GRSTSVYBGRAGIISQMDSLMDSTGPSASMANAPSPVRNNRVYLNPRASLHGGMST 715
QY 578 SIFSKFTSKFYRRNLNBPESKDRVETLRPHVVGSGGNDKEKEFREAKPSSLREFTWSMT 637
Db 716 STTKR-QKQILNETGMPVPDKN-----STSPSKSTDKLDPIKPYFLKGLFVSST 763
QY 638 TSSMEPMEHREIKVLDANSQ-SLHEKMLLCMH-----GTPGHEDPYQ----- 683
Db 764 TSTXSTESIQDLIRVGMGLDIEYKEIKGG--ACLVKPGQIRTPYTKSTVHTRRKPSYG 821
QY 684 -----MEMEYCKLPRLSLNGVRFKRISGTMARFI 714
Db 822 SNSTTDSYGSVPDTPVDDNGESPASNLAFBIYIVKPIISLNGVSTHRISGNSWQYKTL 881
QY 715 ASKIANEIKL 724
Db 882 ASRIINEIKL 891

RESULT 10
A38903
protein kinase 1 - fission yeast (Schizosaccharomyces pombe)
CISpecies: Schizosaccharomyces pombe
CDate: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
JAccession: A38903
RLevin, D.E., Bishop, J.M.
submitted to Genbank, May 1991
AReference number: A38903
AAccession: A38903
A.Molecule type: DNA
A.Residues: 1-891 <LEV>
A.Cross-references: UNIPROT:P22987; GB:M64999; NID:gl73409; PIDN:AAA63577.1; PID:gl73410
RLevin, D.E.; Bishop, J.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8272-8276, 1990

A>Title: A putative protein kinase gene (kin(+)) is important for growth polarity in *S. cerevisiae*
A:Reference number: A36474; MUID:91045979; PMID:2236039
A:Accession: A36474
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-361; 'I', 621-707, 'W', 709-891 <LE2>
A:Cross-references: GB:M36060
C:Genetics:
A:Gene: kin1+
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C:Keywords: ATP, phosphotransferase; serine/threonine-specific protein kinase
P:123-395/Domain: protein kinase homology <KIN>
P:131-139/Region: protein kinase ATP-binding motif

Query Match 21.7%; Score 812.5; DB 2; Length 891;
Best Local Similarity 28.5%; Pred. No. 1e-23;
Matches 243; Conservative 117; Mismatches 317; Indels 177; Gaps 24;

3 SARTPLTLNBRDTEQ-----PTLGLHDSKPSKSNMIRGNATSADQPH-----IGNY 53
83 SSKRPDLASPSRTDHLRVPVSGH-----SYSDKEPRERKRVIGNY 125
54 RLKTTIGKGNPAKYKLAARHILTGKVAVKTI-----DKTQLNSSLQKL 97
126 VLKGTIGAGSGWKVQDAHHLKGTGQPAIKITVRLHPDITKAKAAASAEATKAQSEKNKE 185
98 PRER---IMKVLNHPITVLFETLEKTLVLYMEASGEVDIVANGMKKAKARA 154
186 IRTYREALSTLNLHPYICEARDYINSHYVMEFVVDGQMDYIISHGKKEKQARK 245
155 KFRQVNAVQYCHOKFIYHRDLKAENLLDADNMKIKADFGFNEFTGKNKLDTFGSGPP 214
246 PERQIGALSLYHONSVAHDLKENILISTGDIKIIDGLSNLYRQSLRTFCGSLY 305
215 YAAPELFGQKKYDGPVDVWSGLVILYTVSGSLPFGQNLKELREKRVLRKRYIPYMS 274
306 FAAPBELNAPYIGPEVDVWSFGVILVVLGVCGKFPDQNMALHAKIKKGYVEPYLS 365
275 TDGNNLKKFLILNPSKRGTLKQMKRMANVGHED-----DEKAYVEPLDYKPPR 328
366 SDCKGLLSRLMLVTDPLKRALTEELNLPMMIRNVEGPPASAPRSPITPL-----DPEI 421
329 TELVWSMGY-----TREIQDSLVCGRYNEVMAITYLLGKSSSLBEDDTITLKRPSA-D 382
422 IREMGNDPFGPEPKIYVELTKVISSEAYQSLAKTGFSGNSADKKKSPFEPRIIRAHAD 481
383 LTNSSAPSPSHKYORSVSNP-----KORRSPDAG-----PAIPTSNSYSKYT 426
482 IENPILPSLNMNDIYDAFHPILSIVYVSEBRVYERKGMNRKIAKTPVSSVPQPT 541
427 QSNNAENKRP-----EDRSGRKASSTAKVPASPLPGLERKKTTPPTSTNSVLSTS--- 478
542 SYNRUTLPMPPEVVAAYKGDSPRVSNTSLARRKPLDTE--SHSPSPSATSSIKKPPSS 539
479 -----TNSRNSPLLEBASLQGSJONGKDSAPQORVPVAPASANISSGAPD 528
600 IFRASRRKONKSSSTLQNSAPL-----ETSSQSPTEPKTKPSHKRP---VSYKAKLV 651
529 RTNPPRGVSRSSTFHAQLRQV-----RDOONLPYGV---TPASPSGSGRR 573
652 QSAIGRTSVREGVYAGISSQMDSLNMDSTGPASAMNANAPPSVRNNRVLNPRGASLGHG 711
574 GAGGSISKFTSKVRKLNLEPESKQVETLRPHVVGSGNDKEKEFRKAPRSLRFTW 633
712 RMSTSTNR-OKQILNETGNPVDKN-----STSPSKSTDLIDIKVFLKGLF 759
634 SMKTSMEBNEMMREIRKVLANDANSC--SELHEKYMMLCN-----GTPGHEDFVQ--- 663
760 SVSTTSKSTESIORDLMLVGMGLDIYKIKGCI--ACLYKPOGQITTPKTSVHTTRK 817
684 -----MEMEVCULPRLSLNGVAFKISGTSM 710
818 PSYGSNSTDYSGVDPVPLDNGESPASNLAFEIIYIVKVPILSLGSGVFHNRISGWSQ 877

QY 711 EKNIAASKINELKT 724
DB 878 YKTLASRIINELKT 891

RESULT 11
A26030
serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein YDR477w
C/Species: *Saccharomyces cerevisiae*
C/Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jul-2004
C/Accession: A26030; S69644
R/Celena, J. L.; Carlson, M.
Science 233, 1175-1180, 1986
A>Title: A yeast gene that is essential for release from glucose repression encodes a p
A:Reference number: A26030; MUID:86289463; PMID:3526554
A:Accession: A26030
A:Molecule type: DNA
A:Residues: 1-633 <CEL>
A:Cross-references: UNIPROT:P06782; EMBL:M13971; NID:g172629; PIDN:AAA35058.1; PID:g172
R/Dietrich, F.S.
Submitted to the EMBL Data Library, August 1995
A:Description: The sequence of *S. cerevisiae* cosmid 9410, 8035, 8166, and 9787.
A:Reference number: S69554
A:Accession: S69544
A:Molecule type: DNA
A:Residues: 1-633 <DIE>
A:Cross-references: EMBL:U03050; NID:g927726; PIDN:AA64904.1; PID:g927733; GSPDB:GN000
C/Genetics:
A:Gene: SGD:SNF1; MIPS:YDR477w
A:Cross-references: SGD:S0002885; MIPS:YDR477w
A:Map position: 4R
C/Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonine-phosphate
A:Note: required for expression of glucose-repressed genes in response to glucose depriv
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP, autophosphorylation; magnesium; nucleus; phosphoprotein; phosphotransf
P:53-306/Domain: protein kinase homology <KIN>
P:61-69/Region: protein kinase ATP-binding motif
P:184,103,177,179/Active site: Lys, Glu, Asp, Lys #status predicted
P:182,186/Binding site: magnesium (Aen, Asp) #status predicted
P:210/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predicted

Query Match 21.3%; Score 797.5; DB 1; Length 633;
Best Local Similarity 36.0%; Pred. No. 2.6e-23;
Matches 190; Conservative 94; Mismatches 163; Indels 81; Gaps 12;

39 NSATSDQPHIGNYVLLKTTIGKGNPAKYKLAARHILTGKVAVKTIIDKQQLNSSLQ-KL 97
41 NPKSSLDAGHIGNYVITKTLGSGFGKVLATHTTGQVVALKITINKVLAWSDMQGR1 100
98 FREVRIMKVLNHPNIYKLEVEITETKTLVLYMEVYASGEVFDIVANGMKKAKARA 157
101 ERELISVLRILRHRIHILKLVDSIKSKEIIMVEIYA-GNELFDYIVGRDKMSDEARFFQ 159
158 QVVSAYQYCHOKFIYHRDLKAENLLDADNMKIKADFGFNEFTGKNKLDTFGSGPPYAA 217
160 QILSAVEYCHRHKIVHRDLKPENLIDENHNVKIAIDFGLSINMTDGNPLFTSGSPYAA 219
218 PELFGQKKYDGPVDVWSGLVILYTVSGSLPFGQNLKELREKRVLRKRYIPYMSDTC 277
220 PEVTSKLTAGPEVDVWSGVILYVLCRLRPDDSDISIVLFXNISNGVTLTKPKFSPGA 279
278 ENLKKFLILNPSKRGTLKQMKRMANVGHEDDELKPYVEPLP-----DYKDP 326
280 AGIKKMLVNPINRISIHINQDDWFKVDLPREYLLRPDLKRPBENENNDSKKGGSSP 339
327 RRTY-----LMSMGYTRFETIQSLVQGR---YNVMAITYLLGKSSSLBEDDTIT 374
340 DNDIEDNVLNLLSSITMGYEKEIYESLESSBEDTPAFNEIRDAYVM----- 385
375 LKRPESADLTNNSAPSPSHKYORSVSNPKQRFPDQAPALPTSNSYSKTKQSNNAENK 434

Db 386 IKENKSLIKOMKANKSDELDLTLSSQSP-----PFFQOOSKSHQSQYDH- 431
Qy 435 RPEEDRESGRKASS--TAKVPASPLPGLERKKTTPPTSTNSVLSTSTNRNSPLLRAS 492
Db 432 --ETAKOHARMAISAITQOFTYHOSPFMDYK--EEDSTVSLPTSL-----PQIHAN 481
Qy 493 LGQASIQNGKDSHTAPQRPVVASPSAHNIISSSGAPDRTNPRGVSSRS 540
Db 482 M-----LAQSPASAKISPLVTYKSKTRMHFGIRSRSS 513

RESULT 12
T20941
hypothetical protein F15A2.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20941
R:Gregory, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19349
A:Accession: T20941
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-887 <full>
A:Cross-references: UNIPROT:Q19469; EMBL:Z70207; PIDD:CAA94127.1; GSPDB:GN00028; CESP:F1
A:Experimental source: clone F15A2
C:Genetic:
A:Gene: CESP.F15A2.6
A:Map position: X
A:introns: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3; 604/2; 684/3; 735/2; 777

Query Match 20.8%; Score 778.5; DB: 2; Length 887;
Best Local Similarity 29.5%; Pred. No. 1.9e-22;
Matches 221; Conservative 139; Mismatches 273; Indels 115; Gaps 23;

Qy 49 HIGNYRLKLTIGKGNFAKVLARHILTGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLN 108
Db 16 YCGPYKLEKTLGKQGTGLVKTGHCITGRKVALKIYVKEKLSVLOKVEREIAIMKLE 75
Qy 109 HPNIVKLFVYIEKTLIYVMEYASGGEVFDYLVAHGRMKEKARAKPRQVSAVOYCHQ 168
Db 76 HPVHLHYDYVENKTYLLLEHVSQGEFLDYLVKGRMLMSKEARFRRQIISALDFCHA 135
Qy 169 KFIYHRDLKAEENLLDADNMIKIADPGFSNEFTFGKLDTPFGSPPYAAPBELFOGKKYDG 228
Db 136 HNICHRDLKPEENLLDERNNIKVADFGMASLQVBSMLTSCSPHYACSEVIRGEKYDG 195
Qy 229 PEVDVMSLGVILYTLVSGSLPFDGQNLKELREVLNGKRIIPYMSDTCENLLKKEFLIN 288
Db 196 RKADVMSGCVILYALVGLPFDQDNLNLEKVKSGVPHIPIHFVADVOSILRAMIEVD 255
Qy 289 PSKRGTLKQIMKRMNM-VGHEDEL-----KYYEPLPYKQPRRTTELMVNSG--Y 337
Db 256 PGRYSIADYFKIPWMSGTTKADPELELPWSQVQTHVPIGSEDSIDPDVLRHNNCGGCKP 315
Qy 338 TREIEIDSLVGRYRN-EVMATYLLLGKSGSE--LEQPT--ITLK-----PRPSADLN 385
Db 316 DKQKLNELISPGHNTKRYVYFLDLKRRRRPAQEDDTETLVKGAQNNDPPKQRTDSR 375
Qy 386 SS-----APSPSHVQSVSANPKQRRPSDAQPAIPTSNYSKK--TQSNNAENR 435
Db 376 TSHYPMGSIADGSPINPRKTYGNQSGRHSLSGSPTESPRSTDTDLGSSSSGYSAR 435
Qy 436 PEEDRESGRKASSTAK-----VPASPLPGLF-----RKKTPPTSTNSVLSTINRSN 484
Db 436 AGEDRRGRSASSTNSYHYTQPVDPOTLAEARHVRDAOERRESRDSGSGSRKESKD 495
Qy 485 SPLLEPASLQASIQNGKDSHTA--PORVVASPSAHNIISSSGAPDRTNPRGVSSRSR 542
Db 496 R---SRKASASSSCKQKDASTSSVPHKYPSPVMSASVVVSSSTMNSTN-----SSTNSL 547
Qy 543 HNGQLRQVBDQNLPHYGVTPASPSGHSQGRGASGISFSKF--TSKFRVARNINPESSKDR 600

Db 548 IANNSQTSIGSTGFW-----RKLNINIKNSFLGTGPRFRKRN----- 587
Qy 601 VETLARVHVVGSGNDKEKEPREAKPRSLRFTW--SMKTTSSMEPEEMREIRKVLANS 658
Db 588 -----GTMSDESDQMDITTD-LVKSNPFGSLASSMVERDDTHCVQGGTILNS 637
Qy 659 COSELHEKYMLL--CMHGTPGHEDF-----VQWMEVCKLP-RLSLIN 697
Db 638 IKALIRAPLQIHELHSHSVVQGNCFREYKRGPTVGVSVFSRGIKMNVDIIPSPQGVIA 697
Qy 698 G-----VREKRISGTSMAFKNIASKIA 719
Db 698 GETPTVYVQFVLLAGPVRFRKRLVEHLS 725

RESULT 13
S52244
p69g3 protein - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 16-Aug-2004
C:Accession: S52244
R:Rogni, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg3, selected by differential screening encodes a new *Xenopus* protein kin
A:Reference number: S52243
A:Accession: S52244
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-651 <ROG>
A:Cross-references: UNIPROT:Q91821; EMBL:Z17205; NID:g609283; PIDD:CAA78913.1; PID:g6092
C:Keywords: ATP
F:11-265/Domain: protein kinase homology
F:19-27/Region: protein kinase ATP-binding motif

Query Match 20.8%; Score 776.5; DB: 2; Length 651;
Best Local Similarity 30.8%; Pred. No. 1.6e-22;
Matches 217; Conservative 124; Mismatches 266; Indels 97; Gaps 20;

Qy 53 YELLTIGKGNFAKVLARHILTGKEVAVKIIDKTQLNSSSIQKLFREVRIMKVLNHPNI 112
Db 13 YELHETVGGFAKVKLASHILTGKVALIKIMDKESL-GDLPKYKTEIDAMKQLSHQHV 71
Qy 113 VGLFVYIEKTLIYVMEYASGGEVFDYLVAHGRMKEKARAKPRQVSAVOYCHQKTI 172
Db 72 CRLYHVIETPKKIFWVLEPCGGELFDYIIAKDRLTEEARVFPQIVSAVAVYHSQGYA 131
Qy 173 HNDLKAENLLDADNMIKIADPGFSNEFTFG--NKLDTPFGSPPYAAPBELFOGKKYDGP 230
Db 132 HNDLPEENLLIDEDQNLKIDPGLCAKPKGLDTHILMTCCSPVYAAABELIQKAYIGSE 191
Qy 229 PEVDVMSLGVILYTLVSGSLPFDGQNLKELREVLNGKRIIPYMSDTCENLLKKEFLIN 288
Db 221 VDVMSLGVILYTLVSGSLPFDGQNLKELREVLNGKRIIPYMSDTCENLLKKEFLIN 290
Qy 221 KRGTLKQIMKRMNM-VGHEDELKPYVPLPDYADPRTELMVNSGTYREIIDSIVGR 350
Db 192 ADIWMGVLVYALMCGVLPFDQDNLNLEKVKSGVPHIPIHFVADVOSILRAMIEVD 251
Qy 256 PGRYSIADYFKIPWMSGTTKADPELELPWSQVQTHVPIGSEDSIDPDVLRHNNCGGCKP 315
Db 252 KRITVKNLHPWLMHGGSCVEMOSKYPILGYIDEDCVTELSVYKYSRTSTTLISWS 311
Qy 351 YNEVATYLLLGKSGSELEPTITLK-PRPSAD--LTNSAPSPSHKV-----QSVSAN 402
Db 312 YDHTIASYLHLHSSKS--HGKAVRLKPLAVGDAVTSFKELRKSULDPEEPNGEIAVY 369
Qy 403 PKQRRPSDAQPAIPTSNYSKKTQSNNAENKREEDRESGRKASSTAKVPASPL----- 457
Db 370 FGSMDPFSDE-----ELFSEDPYSSFEHPTKREYKGLRBNSDVASATVFNAML 421
Qy 458 -----PGLERKKTTPPTSTNSVLSTINRSR--SPLLEPASLQASIQNG 500
Db 422 GTKKKIKRTVIGQIPGKMSPCT--OHKGLLLGGGRMKRRVYSPILIKTLKQKRIKSIQ 478
Qy 501 GKDSAPQRPVVASPSAHNIISSSGAPDRTNPRGVSSRSSTFHAGQLRQVADQNLPHYGV 560

Db 479 KGRQLKSLVLP-GEPFANVLS-----PER-----RCKSVLELDNQHH-- 514
Qy 561 TPASPSGSHSGCRKASGISFSTKSTFVRRLNLPESKDRVETLRPHVVGSGGNDKEKE 620
Db 515 -----IDSAQKKKGA--KVFQS-----LERGLDK-----MITMLTP-----SKRGKY 549
Qy 621 PREAKPSRLPRTWMTKTTSSMEPMEMREIRKVLNANSCSELEKXMLLCHMTCPGHD 680
Db 550 TREB-PKKLRNHNVTNTTNVPEQLNQIVRLVPSKGV-DYVKGITLTKCKTQSDPKV 607
Qy 681 FVQWEMEVCKLPRLSLNGVPRKISGTSMAPKNIASKIANELK 724
Db 608 TMQPELEVCQLSKSEVVGIRQRRLKGDAMVYKRLVEIDILSSCKV 651

RESULT 14

872513
C:Species: Kluyveromyces marxianus var. lactis, Candida bphaerica
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: 572513
R:Ggffintl, P.; Flcarell, A.; Domini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
Curr. Genet. 29, 316-326, 1996
A:Title: FOG1 and FOG2 genes, required for the transcriptional activation of glucose-reg
A:Reference number: 872513, MUID:96171514, PMID:8538052
A:Accession: 872513
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6d2 <GOF>
A:Cross-references: UNIPROT:P87209
A>Note: the source is designated as Kluyveromyces lactis
C:Gene: FOG2
C:Function:
A:Description: probably involved in the regulation of glucose-repressible gene expresio
C:Superfamily: AMP-activated protein kinase; protein kinase homology
P:33-286/Domain: protein kinase homology <Kin>

Query Match 20.7%; Score 775; DB 2; Length 602;

Best Local Similarity 37.3%; Pred. No. 1,7e-22;
Matches 187; Conservative 83; Mismatches 157; Indels 74; Gaps 12;

Qy 27 KPSKSMWIRGNATSDAEQPHNGRLKTKTGKGFAPYKLABHILTGKEVAVKIDK 86
Db 9 QPHGSGQGHNRQRLTHRAQGNHGXQIITKEGSGFGKVKLAHISTOKVALKINK 68
Qy 87 TOLNSSLQ-KLFEVRIMKVLNPNIVKLFEVETETKTLVLMVEYASGGEVPDYLAHG 145
Db 69 KVLAKSMQGRIEREISYLRILRPHILKLYDKSKDEITIMVEYA-GNELFDYIVQRD 127
Qy 146 RMKEKEARAFQVSAVOYCHQKFIYHRDLKAEMLLDADMNIKIADFGESNEFTGK 205
Db 128 KMPQEARRFQOITISAVDYCHRHKIVHRDLKPEMLLDLHNLVAKIDFGLSNIMTDGNF 187
Qy 206 LDTFGSGPPYAAPLFGQKTYDPEYVWLSGLVLTIVSGSLPFDQGNLKELEKRLRG 265
Db 188 LKTSQSGSPNAAAPVIGKLYAGPEVWVSGVLLYMLCRRLPFDDESIPLVFKINSNG 247
Qy 266 KYRIPFWSTDCBULLKKFLILNPSKRGTLKQIMKDMVMVGHEDDELKPYVEPLPYKD 325
Db 248 VYTFNPLSGAASLTKMLIVNVRITVHEIMQDMFKV-----DLDPYLV 295
Qy 326 P-----RTE-----LMVSGYTRREIDQSLVGQR-----YNE 353
Db 296 PAESTHQENSESKTEDGSPVLELIDSLVQTLSTMTGVDVDEIVALESDHPSLNE 355
Qy 354 VMATYLLLGYSSELEDDITLKRPASADLTNSAPSPSHKVGQSVSANP--KORRSDQ 411
Db 356 IRDAYQLI--KENNLINDIKVNRQGSNDLDTFLSQSP--TFEQSLHAPGSKNRH---- 408
Qy 412 AGPAIPTSNYSKTKQGSNNANENKRPEDRESGRKASSTAKVPASPLGLERKKTTPPTST 471

Db 409 -----SHRSKRTQORTQYHYNGSGD-----GDSTIALPSPLEQIHR-----A 449
Qy 472 NSYLTSTYTRSKNSPLERAS 492
Db 450 NMVAGSGQAAPAKISPLSVKKS 470

RESULT 15

T52633
N:Alternate names: SNF1 protein kinase omolog AKIN11
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52633
R:Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machl
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A:Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein k
A:Reference number: 225116, MUID:99238528, PMID:10220464
A:Accession: T52633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <BHA>
A:Cross-references: UNIPROT:P92958; EMBL:X99279; PIDN:CAA67671.1
A:Experimental source: cultivar Columbia
C:Gene: AKIN11
C:Function:
A:Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated,
complements SNF1 mutations in yeast
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 20.3%; Score 757.5; DB 2; Length 512;

Best Local Similarity 42.9%; Pred. No. 6.6e-22;
Matches 152; Conservative 74; Mismatches 99; Indels 29; Gaps 7;

Qy 37 GRNSATSDAEQPHNGRLKTKTGKGFAPYKLABHILTGKEVAVKIDTOLNSSLQ-Q 95
Db 9 GNNGVESI-----LPNFKLGKTLGIGSGFGKVKLAHNVVGHKVALIKILNRRKIKNMEMEE 63
Qy 96 KLFEVRIMKVLNPNIVKLFEVETETKTLVLMVEYASGGEVPDYLAHGMRKEKARAK 155
Db 64 KYRREIKILRLFMHPIHRIQVEYIETSDIYVMEVYKSGELFDYIVKGRQLQDEARNF 123
Qy 156 FROVSAVOYCHQKFIYHRDLKAEMLLDADMNIKIADFGESNEFTGKLDTFGSGPPY 215
Db 124 FQIISGVEXCHRMVYHRDLKPEMLLDLDRCNKIADFGLSVWMDGHLKTSQSGSPNY 183
Qy 216 AAEPLQGGKYDPEVDWVSLGVLTYTVSGSLPFDQGNLKELEKRLRGKYIIPYMTST 275
Db 184 AAEVIVSGKLYAPPEVDWVSGVILYALLCGTLPPDENIPNLFKIKGIGIYTLPSHLSS 243
Qy 276 DCENLKKFLILNPSKRGTLKQIMKDMVMVGHEDDELKPY--VEPLPYKDPBR----- 328
Db 244 EARDLIPRMLIVDPVGRITIPRIQRHWPQT-----HLPRYLVSP--PDVEAQAKINEE 297
Qy 329 -TELMVSGYTRREIDQSLVGQRYNEVMATYLL-----GYKSSLESDGT 372
Db 298 IYQEVVNMGFRNQVLESILNRFQNDATVYVYLLDNRRFRVPAGYLESSEFQETT 351

Search completed: February 26, 2005, 17:52:13
Job time : 50 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 17:34:27 ; Search time 177 Seconds

(without alignments)
2094,606 Million cell updates/sec

Title: US-10-760-407-2

Perfect score: 3737

Sequence: 1 MSBARTPLPLTNERDTEQPT.....SGTSMAFKNIASKIANELKL 724

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3654	97.8	722	2	008679
2	3654	97.8	722	2	06PDR4
3	3647.5	97.6	719	2	068A18
4	3624	97.0	778	2	096HB3
5	3598	96.3	888	2	08BR95
6	3566	95.4	691	2	096R00
7	3515	94.1	745	2	015524
8	3504	93.8	755	2	07KZ17
9	3467	92.8	774	1	MRK2_MOUSE
10	3195.5	85.5	776	2	07ZY17
11	3188	85.3	785	2	08QGV3
12	3027	81.0	780	2	08Q4P1
13	2561	68.5	795	2	08VH5
14	2555	68.4	793	2	086F78
15	2546	68.1	795	2	09P012
16	2523.5	67.5	792	2	061N17
17	2493	66.7	771	2	069Z17
18	2398.5	64.2	744	2	09JKE5
19	2398.5	64.2	776	1	MRK3_HUMAN
20	2395.5	64.1	870	2	09P251
21	2377	63.7	729	2	09JKE4
22	2374	63.6	725	2	08Q4T2
23	2374	63.5	797	2	08VH0
24	2078	55.6	722	2	08Q2W0
25	1950	52.2	659	2	086T78
26	1940.5	51.9	752	1	MRK4_HUMAN
27	1938.5	51.9	752	2	08C1F4
28	1932.5	51.7	752	2	08N3J7
29	1902	50.9	594	2	06PA64
30	1902	50.9	704	2	07PKD5
31	1894	50.7	938	2	Q9V8V8

32	1878.5	50.3	638	2	096SM9	Q96SW9 homo sapien
33	1830.5	49.0	905	2	07KRK5	Q7KR5 drosoophila
34	1826	48.9	1138	2	07KRK3	Q7KR3 drosoophila
35	1820.5	48.7	1075	2	095U75	Q95U75 drosoophila
36	1818	48.6	1066	2	08MVX0	Q8MVX0 haemochus
37	1782.5	47.7	1096	2	017368	Q17368 caenorhabd
38	1771.5	47.4	1192	2	09TW45	Q9TW45 caenorhabd
39	1765.5	47.2	1192	2	017346	Q17346 caenorhabd
40	1710.5	45.8	966	2	08MVX2	Q8MVX2 haemochus
41	1587	42.5	634	2	080T81	Q80T81 mus musculu
42	1556.5	41.7	1046	2	07YU80	Q7YU80 drosoophila
43	1552	41.5	993	2	07KRK4	Q7KR4 drosoophila
44	1551	41.5	833	2	06NDP6	Q6NDP6 drosoophila
45	1550.5	41.5	1058	2	Q963B5	Q963B5 drosoophila

ALIGNMENTS

RESULT 1
ID 008679 PRELIMINARY; PRT; 722 AA.
AC 008679;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Serine/threonine Kinase.
GN Name=mark2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=97262070; Pubmed=9108484; DOI=10.1016/S0092-8674(00)80208-1;
RA Drewes G., Ebnech A., Preuse U., Mandelkow E.;
RT "MARK - a Novel Family of Protein Kinases that Phosphorylate
RT Microtubule-associated Proteins and Trigger Microtubule Disruption."
RL Cell 89:297-308 (1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Drewes G., Ebnech A., Preuse U., Mandelkow E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; Z83869; CAB06295.1; -.
DR HSSP; P24941; IOIO.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011772; Kinase_Cterm.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR000449; UBA.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00627; UBA; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_STR; 1.
DR PROSITE; PS0030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 722 AA; 80871 MW; 2CBAPD1C38007ECC CRC64;

Query Match 97.8%; Score 3654; DB 2; Length 722;
Best Local Similarity 97.8%; Pred. No. 1.8e-170;


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Db 241 YTLVSGSLPFDGQNLKRLRVLRGKRIIPFYWSTDCENLKKFLINPSKRGTLBQIMK 300
Qy 301 DRMNANGHEDEDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Db 301 DRMNANGHEDEDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEBDDITTLKRPADLTNSGAPSPSHKVQSVSANPKORSSDOAVPALPTSN 420
Db 361 LGYKSSLEBDDITTLKRPADLTNSGAPSPSHKVQSVSANPKORSSDOAVPALPTSN 420
Qy 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLGLEKKTTPTSTNSVLTSTN 480
Db 421 SYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLGLEKKTTPTSTNSVLTSTN 480
Qy 481 RSRNSPLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGABDRTNPRGVSSRS 540
Db 479 RSRNSPLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGABDRTNPRGVSSRS 538
Qy 541 TFHAGQLRQVRDOONLPYGVTPASPSGHSQGRGASGISFTSKFVRRNLNBPESKDR 600
Db 539 TFHAGQLRQVRDOONLPYGVTPASPSGHSQGRGASGISFTSKFVRRNLNBPESKDR 598
Qy 601 VETLRPHVVGSGNDKXKEEFREAKPRSLRFTWSMKTTSMBPNEMMRIRKVLNANSCQ 660
Db 599 VETLRPHVVGSGNDKXKEEFREAKPRSLRFTWSMKTTSMBPNEMMRIRKVLNANSCQ 658
Qy 661 SBLHEKXTMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRLSGTSMAPKQIASKIAN 720
Db 659 SBLHEKXTMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRLSGTSMAPKQIASKIAN 718
Qy 721 ELKL 724
Db 719 ELKL 722
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RESULT 3

068A18 PRELIMINARY; PRT; 719 AA.

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AC 068A18;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DN Serine/threonine kinase.
GN Name=mark2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11)
RP SEQUENCE FROM N.A.
RC TISUB=Kidney;
RA Sugiyama A., Inoue H., Oka M.;
RT "Homo sapiens mRNA."
RL Submitted (JUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB188493; BAD3741.1; -
DR GO; GO:0016301; F:Kinase activity; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00669; Pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKIC; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
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DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0030; UBA; 1.
KW Kinase.
SQ SEQUENCE 719 AA; 80646 MW; EC39154CF73E958 CRC64;
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Query Match 97.6%; Score 3647.5; DB 2; Length 719;
Best Local Similarity 98.1%; Pred. No. 3.7e-170;
Matches 711; Conservative 4; Mismatches 3; Indels 7; Gaps 2;

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Qy 1 MSSARTPPLPTLNERDTEOPTLGHLDSPSSKSMNIRGRSATSADQPHIGNYRLKTTIG 60
Db 1 MSSARTPPLPTLNERDTEOPTLGHLDSPSSKSMNIRGRSATSADQPHIGNYRLKTTIG 60
Qy 61 KGNFAKYLARHILTGKEVAVKIIDTQLNSSLQCLFREVRIMKVLNBNIVKLEFVIE 120
Db 61 KGNFAKYLARHILTGKEVAVKIIDTQLNSSLQCLFREVRIMKVLNBNIVKLEFVIE 120
Qy 121 TEKTLVMEYASGGVFPYLVAGHMKKEAKRQVSAVOYCHQKFIYHRDLKAEN 180
Db 121 TEKTLVMEYASGGVFPYLVAGHMKKEAKRQVSAVOYCHQKFIYHRDLKAEN 180
Qy 181 LLLDADNLIKADFGSNEFTFGNKLDTFCGSPYAAPLFGQKTDGPEVDVMSLGVIL 240
Db 181 LLLDADNLIKADFGSNEFTFGNKLDTFCGSPYAAPLFGQKTDGPEVDVMSLGVIL 240
Qy 241 YTLVSGSLPFDGQNLKRLRVLRGKRIIPFYWSTDCENLKKFLINPSKRGTLBQIMK 300
Db 241 YTLVSGSLPFDGQNLKRLRVLRGKRIIPFYWSTDCENLKKFLINPSKRGTLBQIMK 300
Qy 301 DRMNANGHEDEDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Db 301 DRMNANGHEDEDELKPYVEPLPDYKDPRTTELWVSMGYTREIEIDSLVGQRVNEVMATYLL 360
Qy 361 LGYKSSLEBDDITTLKRPADLTNSGAPSPSHKVQSVSANPKORSSDOAVPALPTSN 420
Db 361 LGYKSSLEBDDITTLKRPADLTNSGAPSPSHKVQSVSANPKORSSDOAVPALPTSN 420
Qy 420 NSYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLGLEKKTTPTSTNSVLTST 479
Db 420 NSYSKKTQSNNAENKRPEDRESGRKASTAKVPASPLGLEKKTTPTSTNSVLTST 479
Qy 480 NRSRNSPLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGABDRTNPRGVSSR 539
Db 480 NRSRNSPLERASLGGASLQNGKOSTAPQVVPASPSAHNISSSGABDRTNPRGVSSR 539
Qy 540 STFHAGQLRQVRDOONLPYGVTPASPSGHSQGRGASGISFTSKFVRRNLNBPESKDR 599
Db 541 STFHAGQLRQVRDOONLPYGVTPASPSGHSQGRGASGISFTSKFVRRNLNBPESKDR 599
Qy 600 RVETLRPHVVGSGNDKXKEEFREAKPRSLRFTWSMKTTSMBPNEMMRIRKVLNANSC 659
Db 600 -----RPHVVGSGNDKXKEEFREAKPRSLRFTWSMKTTSMBPNEMMRIRKVLNANSC 654
Qy 660 QSLIHKXTMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRLSGTSMAPKQIASKIA 719
Db 655 QSLIHKXTMLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRLSGTSMAPKQIASKIA 714
Qy 720 NELKL 724
Db 715 NELKL 719
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RESULT 4

096HB3 PRELIMINARY; PRT; 778 AA.

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AC 096HB3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MARK2 protein (Fragment).
GN Name=MARK2;
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
 RA Diatchenko L., Marzista K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stropeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Rha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Besak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyanski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.,
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC008771; AA08771.2; -
 DR PIR; G01025; G01025.
 DR HSP; P24941; 1010.
 DR Intact; Q96HB3; -
 DR Genew; HENC3332; MARK2.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001772; Kinase_Cterm.
 DR InterPro; IPR011009; Kinase_Like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR000449; UBA.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00627; UBA; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0220; S_TKC; 1.
 DR SMART; SMO0219; TYKC; 1.
 DR SMART; SMO0165; UBA; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00300; UBA; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER
 SQ SEQUENCE 778 AA; 86868 MW; 557691C4CDB617A CRC64;
 Query Match 97.0%; Score 3624; DB 2; Length 778;
 Best Local Similarity 91.6%; Pred. No. 5,7e-169;
 Matches 713; Conservative 1; Mismatches 0; Indels 64; Gaps 3;

QY 11 LNERDTPQPTGLHDSRSSKSNIRGNATSADDEPHIGNYLLKTIGKGNFAKYLA 70
 DB 1 LNERDTPQPTGLHDSRSSKSNIRGNATSADDEPHIGNYLLKTIGKGNFAKYLA 60

QY 71 RHILTGKAVAKIIDKQNLNSSLQKLFREYRIMKVLNHPNIVKLFEVITEKTLVYME 130
 DB 61 RHILTGKAVAKIIDKQNLNSSLQKLFREYRIMKVLNHPNIVKLFEVITEKTLVYME 120
 QY 131 YASGEVEFDYVAHGRMEKEKARAFQVSAVOYCHQKFTVHRDLKAENILLDADNIX 190
 DB 121 YASGEVEFDYVAHGRMEKEKARAFQVSAVOYCHQKFTVHRDLKAENILLDADNIX 180
 QY 191 IADPGPSNEFTFGKLDLTFCCSPPIAABELQKKYDDPEVDWMSGLVTLVSGSLPF 250
 DB 181 IADPGPSNEFTFGKLDLTFCCSPPIAABELQKKYDDPEVDWMSGLVTLVSGSLPF 240
 QY 251 DQONLKEIRERYLRGKXVIFPFYMSDCENLKKFILLPSKRGTEQIMKRMNVGHED 310
 DB 241 DQONLKEIRERYLRGKXVIFPFYMSDCENLKKFILLPSKRGTEQIMKRMNVGHED 300
 QY 311 DELKPYVEPLPYKDPRTTELNVSGYTRREIQDSLVGQRYNEVATYLLIGYSSLEIG 370
 DB 301 DELKPYVEPLPYKDPRTTELNVSGYTRREIQDSLVGQRYNEVATYLLIGYSSLEIG 360
 QY 371 DTTTLKPRPSADLTNSAPSPSHKQSVSANPKORRRSDQ-AGPAIFTSNSYKKTQSN 429
 DB 361 DTTTLKPRPSADLTNSAPSPSHKQSVSANPKORRRSDQ-AGPAIFTSNSYKKTQSN 420
 QY 430 NAENKRPEDRESGRKASTAKVPASPLGLERKKTTPSTNSYLSSTNRSRNPYLE 489
 DB 421 NAENKRPEDRESGRKASTAKVPASPLGLERKKTTPSTNSYLSSTNRSRNPYLE 480
 QY 490 RASLGQASIQNGKD----- 503
 DB 481 RASLGQASIQNGKDSLTPGSPASTASAAVASAPRQHQKSMGSAVHPNKAAGLPTE 540
 QY 504 -----STAPQRPVAPSPSAHNTSSSGGAPDRPNPFGVSSRSTPHAGOLROYDOON 555
 DB 541 SNCEVPRPSTAPQRPVAPSPSAHNTSSSGGAPDRPNPFGVSSRSTPHAGOLROYDOON 600
 QY 556 LPYGVTPAPSPGSHSGGRGASGISFSKFTSKFV-----RRNINEBSKDRVETLRP 606
 DB 601 LPYGVTPAPSPGSHSGGRGASGISFSKFTSKFVRRNINEBSKDRVETLRP 660
 QY 607 HVGSGGNDKEXEKEPREAKRSLRTTWSMKTTSMEPNEMREIRKVLTDANCCSELEHX 666
 DB 661 HVGSGGNDKEXEKEPREAKRSLRTTWSMKTTSMEPNEMREIRKVLTDANCCSELEHX 720
 QY 667 YMLCWHGTPGHEDPFQWMEYCKLPRLSLNGVRFKRSISGTSMAPFNIAISKIANEKL 724
 DB 721 YMLCWHGTPGHEDPFQWMEYCKLPRLSLNGVRFKRSISGTSMAPFNIAISKIANEKL 778
 RESULT 5
 ID Q8BR95 PRELIMINARY; PRT; 888 AA.
 AC Q8BR95;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
 DE enriched library, clone: B13006516 product: ELKL motif kinase, full
 DE insert sequence. (fragment).
 GN Name=Mark2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:13-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1036/35055500;
 RA RIKEN FANTOM Consortium; PubMed=11217851; DOI=10.1036/35055500;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA The RIKEN Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Ozaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 Sumi T., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
 Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsumoto M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 Ozaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN (6)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA Aachari J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 Horii F., Imclanti K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Ozaki Y.,
 Saito R., Saitoh H., Sakai C., Sakai S., Sakazume N., Sano H.,
 Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK045329; BAC32312.1; -.
 DR HSSP; P24941; IOIO.
 DR MGD; MGI:96638; Mark2.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0004674; P:Protein Serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; P:Transferase activity; IEA.
 DR GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011772; Kinase Cterm.
 DR InterPro; IPR011009; Kinase Like.
 DR InterPro; IPR000719; Prot. Kinase.
 DR InterPro; IPR002290; Ser_Thr_Kinase.
 DR InterPro; IPR008271; Ser_Thr_Kinase.
 DR InterPro; IPR000449; UBA.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00637; UBA; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE; PSS0030; UBA; 1.
 KR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 888 888
 SQ SEQUENCE 888 AA; 98822 MW; 07C8F23520F80CD CRC64;
 Query Match 96.3%; Score 3598; DB 2; Length 888;
 Best Local Similarity 90.8%; Pred. No. 1,3e-167;
 Matches 704; Conservative 9; Mismatches 6; Indels 56; Gaps 2;
 QY 1 MSSARPLPTLNEDTQPTLGLHDSKPSKSNMIRGNSATSADQPHIGNRLKLTIG 60
 DB 1 MSSARPLPTLNEDTQPTLGLHDSKPSKSNMIRGNSATSADQPHIGNRLKLTIG 60
 QY 61 KGNPAKYLARHLITGGEVAVKIIDKTQLNSSLQQLFRERIRIMKVLNHNIVKLFVIE 120
 DB 61 KGNPAKYLARHLITGGEVAVKIIDKTQLNSSLQQLFRERIRIMKVLNHNIVKLFVIE 120
 QY 61 KGNPAKYLARHLITGGEVAVKIIDKTQLNSSLQQLFRERIRIMKVLNHNIVKLFVIE 120
 DB 61 KGNPAKYLARHLITGGEVAVKIIDKTQLNSSLQQLFRERIRIMKVLNHNIVKLFVIE 120
 QY 121 TEKTLVLMVEYASGEVFDVLVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGEVFDVLVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 QY 121 TEKTLVLMVEYASGEVFDVLVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 DB 121 TEKTLVLMVEYASGEVFDVLVHGRMKKEAKAPQVAVAYQCHQKFTVHRDLKAEN 180
 QY 181 LLLDADNMNLIKADFGFSNEFTFGNKLDTFCGSPPYAAPLFGQKKVDGPEDVWSLGIVL 240
 DB 181 LLLDADNMNLIKADFGFSNEFTFGNKLDTFCGSPPYAAPLFGQKKVDGPEDVWSLGIVL 240
 QY 241 YTVVSGSLPPDQGNLKLRRVLRGKRIFFYVSTDCENLLKFLINPBRKGLTDIMK 300
 DB 241 YTVVSGSLPPDQGNLKLRRVLRGKRIFFYVSTDCENLLKFLINPBRKGLTDIMK 300
 QY 301 DRMMVNGHEDDELKPYVEPLPDYKDPRTETLWVSMGTREIIDSLSVGQRYNEVMAAYLL 360
 DB 301 DRMMVNGHEDDELKPYVEPLPDYKDPRTETLWVSMGTREIIDSLSVGQRYNEVMAAYLL 360
 QY 301 DRMMVNGHEDDELKPYVEPLPDYKDPRTETLWVSMGTREIIDSLSVGQRYNEVMAAYLL 360
 DB 301 DRMMVNGHEDDELKPYVEPLPDYKDPRTETLWVSMGTREIIDSLSVGQRYNEVMAAYLL 360
 QY 361 LGYKSELEBDITTLKPRPSADLTNSAPSPSHKVORVSNAPKORFSDQAGPAIPTSN 420
 DB 361 LGYKSELEBDITTLKPRPSADLTNSAPSPSHKVORVSNAPKORFSDQAGPAIPTSN 420
 QY 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLEKKTTPTESTNSVLSSTN 480
 DB 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLEKKTTPTESTNSVLSSTN 480
 QY 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLEKKTTPTESTNSVLSSTN 480
 DB 421 SYKKTQSNNAENKRPEDRESGRKASSTAKVPASPLPGLEKKTTPTESTNSVLSSTN 480
 QY 481 RSNNSPLLRASLGQASIQNGKSLTPMSGRASSTASAAVSAARPROHOKSASAVHPN 538
 DB 481 RSNNSPLLRASLGQASIQNGKSLTPMSGRASSTASAAVSAARPROHOKSASAVHPN 538
 QY 479 RSNNSPLLRASLGQASIQNGKSLTPMSGRASSTASAAVSAARPROHOKSASAVHPN 538
 DB 479 RSNNSPLLRASLGQASIQNGKSLTPMSGRASSTASAAVSAARPROHOKSASAVHPN 538
 QY 504 -----STAPQRPVAPSPAHNISSSGAPDRTPNPRGVSSRSTFPAQ 546
 DB 504 -----STAPQRPVAPSPAHNISSSGAPDRTPNPRGVSSRSTFPAQ 546
 QY 539 KAGGLPTESNCVPRPSTAPQRPVAPSPAHNISSSGAPDRTPNPRGVSSRSTFPAQ 598
 DB 539 KAGGLPTESNCVPRPSTAPQRPVAPSPAHNISSSGAPDRTPNPRGVSSRSTFPAQ 598
 QY 547 LRQVRDQONIPYGVTPASPSGHSQGRGASGSIFFSKFTSKFVRRLNLPESKORVETLRP 606
 DB 547 LRQVRDQONIPYGVTPASPSGHSQGRGASGSIFFSKFTSKFVRRLNLPESKORVETLRP 606
 QY 599 LRQVRDQONIPYGVTPASPSGHSQGRGASGSIFFSKFTSKFVRRLNLPESKORVETLRP 658
 DB 599 LRQVRDQONIPYGVTPASPSGHSQGRGASGSIFFSKFTSKFVRRLNLPESKORVETLRP 658
 QY 607 HVGSGGNDKEKEKEFEPAKRSIRFTMSMTTSMSBENEMRIRIKVLDANSQOSSELEHK 666
 DB 607 HVGSGGNDKEKEKEFEPAKRSIRFTMSMTTSMSBENEMRIRIKVLDANSQOSSELEHK 666
 QY 659 HVGSGGNDKEKEFEPAKRSIRFTMSMTTSMSBENEMRIRIKVLDANSQOSSELEHK 718
 DB 659 HVGSGGNDKEKEFEPAKRSIRFTMSMTTSMSBENEMRIRIKVLDANSQOSSELEHK 718
 QY 667 YMLLCHGTPGHEDFYQWEMEVCKLPRLSLNGVRFKRIISGTSNAFQVIAASKIANE 721
 DB 667 YMLLCHGTPGHEDFYQWEMEVCKLPRLSLNGVRFKRIISGTSNAFQVIAASKIANE 721
 QY 719 YMLLCHGTPGHENFYQWEMEVCKLPRLSLNGVRFKRIISGTSNAFQVIAASKIANE 773
 DB 719 YMLLCHGTPGHENFYQWEMEVCKLPRLSLNGVRFKRIISGTSNAFQVIAASKIANE 773
 RESULT 6
 ID Q96RG0 PRELIMINARY; PRT; 691 AA.
 AC Q96RG0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ser/Thr protein kinase par-1balpha.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2132471; PubMed=11433294; DOI=10.1038/35083016;
RA Sun T.O., Lu B., Feng J.J., Reinhard C., Yan Y.N., Pantl W.J.,
RA Williams L.T.;
RT "PAR-1 is a dishevelled-associated kinase and a positive regulator of
RT Mtc signalling.";
RL Nat. Cell Biol. 3:628-636(2001).
CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR HMBL; AF387638; AAK82368.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR001009; Kinase_Like.
DR InterPro; IPR002290; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR009060; UBA_Like.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 691 AA; 77631 MW; 22168487BCF31BE CRC64;

Query Match 95.4%; Score 3566; DB 2; Length 691;
Best Local Similarity 99.9%; Pred. No. 3.4e-163;
Matches 690; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

34 MIRGNSATSADBOPHIGNYRLTKTGKGNFAVKYLAARHLLTGKEVAVKIIDKTQNLSSS 93
1 MIRGNSATSADBOPHIGNYRLTKTGKGNFAVKYLAARHLLTGKEVAVKIIDKTQNLSSS 60
94 LQKLFEVRIMKVLNHPNIVKLFEVETETKTLVYMEYASGGVFPDYLVAGRMKEKEAR 153
61 LQKLFEVRIMKVLNHPNIVKLFEVETETKTLVYMEYASGGVFPDYLVAGRMKEKEAR 120
154 AKRQVSAVQYCHQKFIYHRDLKAENLLDADMMIKIADPGPSNEFTGKNTDTCGSP 213
121 AKRQVSAVQYCHQKFIYHRDLKAENLLDADMMIKIADPGPSNEFTGKNTDTCGSP 180
214 PYAAPLFOGKKYDGEVDVMSLGVLLYTLVSGSLPFDGQNLKELREYLRGKYRIIPFY 273
181 PYAAPLFOGKKYDGEVDVMSLGVLLYTLVSGSLPFDGQNLKELREYLRGKYRIIPFY 240
274 STDCENLLKKEFLILNSKSGTLEQIMKDMNMGHEDDELKPYVEVLPDYKDPRTLEAV 333
241 STDCENLLKKEFLILNSKSGTLEQIMKDMNMGHEDDELKPYVEVLPDYKDPRTLEAV 300
334 SMGYTREELIODSLVGRVYEVNATYLLLGKSELEGGDTITLKPRESADLTNNSAPSPH 393
301 SMGYTREELIODSLVGRVYEVNATYLLLGKSELEGGDTITLKPRESADLTNNSAPSPH 360
394 KYQRSVSAVQYCHQKFIYHRDLKAENLLDADMMIKIADPGPSNEFTGKNTDTCGSP 453
361 KYQRSVSAVQYCHQKFIYHRDLKAENLLDADMMIKIADPGPSNEFTGKNTDTCGSP 420
454 ASPLBELERKKTTPSTSTSVLSTSTNRSGNSPLERASIGASLNGQSTAPQGVPA 513
421 ASPLBELERKKTTPSTSTSVLSTSTNRSGNSPLERASIGASLNGQSTAPQGVPA 480

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QY 514 SPFAHNISSSGAPDPTNPRGVSSRSTETHAGOLROYRPOONLPGVTPASPBGSGRR 573
DB 481 SPFAHNISSSGAPDPTNPRGVSSRSTETHAGOLROYRPOONLPGVTPASPBGSGRR 540
QY 574 GASGSIFSKFTSKFYVRNINPESSKDVRETLRPHVVGSGANKEKEEPREAKPRSLRFTW 633
DB 541 GASGSIFSKFTSKFYVRNINPESSKDVRETLRPHVVGSGANKEKEEPREAKPRSLRFTW 600
QY 634 SKTTSSMPEPMMREIRVLDANSQSELEHETMLCMHGTPGHEDFYQWEMEVCKLR 693
DB 601 SKTTSSMPEPMMREIRVLDANSQSELEHETMLCMHGTPGHEDFYQWEMEVCKLR 660
QY 694 LSLNGVFRFRIISGTSAFNIASKTANLKL 724
DB 661 LSLNGVFRFRIISGTSAFNIASKTANLKL 691

RESULT 7
ID Q15524 PRELIMINARY; PRT; 745 AA.
AC Q15524;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9839968; PubMed=9730619;
RA Espinosa L., Navaro E.;
RT "Human serine/threonine protein kinase EMK1: genome structure and cDNA
RT cloning of isoforms produced by alternative splicing.";
RL Cytogenet. Cell Genet. 81:278-282(1998).
CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; X97630; CAA66229.1; -.
DR FIR; G01025; G01025.
DR HSBP; P24941; 1010.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR009060; UBA_Like.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 745 AA; 83204 MW; CERA02EBF62B5DP CRC64;

Query Match 94.1%; Score 3515; DB 2; Length 745;
Best Local Similarity 92.3%; Pred. No. 1.1e-163;
Matches 688; Conservative 1; Mismatches 2; Indels 54; Gaps 1;

34 MIRGNSATSADBOPHIGNYRLTKTGKGNFAVKYLAARHLLTGKEVAVKIIDKTQNLSSS 93
1 MIRGNSATSADBOPHIGNYRLTKTGKGNFAVKYLAARHLLTGKEVAVKIIDKTQNLSSS 60
94 LQKLFEVRIMKVLNHPNIVKLFEVETETKTLVYMEYASGGVFPDYLVAGRMKEKEAR 153

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Db      61 LQKLFREVRIMKVLNHNINIKLFEVIEETKTLYLWMEYASGGEVFDLVAHGMRKEAR 120
Qy      154 AKRQVSAVOYCHQKFIYHRDLKAENLLDADNMIIADPGFSNEFTFGNKLDTFCGSP 213
Db      121 AKRQIVSAVOYCHQKFIYHRDLKAENLLDADNMIIADPGFSNETFGNKLDTFCGSP 180
Qy      214 PYAPBELFOGKKTGDEGVNWSLGVILYTLVSSGLPFDGONLKELRARVLRGKRIIPFM 273
Db      181 PYAPBELFOGKKTGDEGVNWSLGVILYTLVSSGLPFDGONLKELRARVLRGKRIIPFM 240
Qy      274 STDCENLLKKFLILNPSKRGTLBOIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTTLMV 333
Db      241 STDCENLLKKFLILNPSKRGTLBOIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTTLMV 300
Qy      334 SMGYTREELQDSLVGQRYNEVMATYLLGYKSSLEBDTITLKRPSADLTNSAPSPSH 393
Db      301 SMGYTREELQDSLVGQRYNEVMATYLLGYKSSLEBDTITLKRPSADLTNSAPSPSH 360
Qy      394 KVQRSVSNAPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKAASSTAKVP 453
Db      361 KVQRSVSNAPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKAASSTAKVP 420
Qy      454 ASPLPGLERKKTTPPTPSTNSVLTSTNRSRNSPLERASLGOASIQNGKD----- 503
Db      421 ASPLPGLERKKTTPPTPSTNSVLTSTNRSRNSPLERASLGOASIQNGKSLTWPGRAS 480
Qy      504 -----STAPQRYVVASPSAH 519
Db      481 TASASAAVSARPRQHKMSASVHPNKASGLPTESNCEVPRPSTAPQRYVVASPSAH 540
Qy      520 ISSSGAPDRITNPPRGVSSRSTFHAQQLROVRDQONLPYGVTPASPSGSGRRGASGS1 579
Db      541 ISSSGAPDRITNPPRGVSSRSTFHAQQLROVRDQONLPYGVTPASPSGSGRRGASGS1 600
Qy      580 FSKFTSKFVRNINPEBSKQDVEITLRPHVYVSGGNDKEKEPREAKRSILFTWSMKTTS 639
Db      601 FSKFTSKFVRNINPEBSKQDVEITLRPHVYVSGGNDKEKEPREAKRSILFTWSMKTTS 660
Qy      640 SMEPNEMMREIRKVLNANSCOSELHEKYMILCMHGTGHDPIVQMEVCKLRLSLNGV 699
Db      661 SMEPNEMMREIRKVLNANSCOSELHEKYMILCMHGTGHDPIVQMEVCKLRLSLNGV 720
Qy      700 RPKRISGTSMAFKNIASKIANELKL 724
Db      721 RPKRISGTSMAFKNIASKIANELKL 745

RESULT 8
07KZ17 . PRELIMINARY; PRT; 755 AA.
AC 07KZ17;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DB 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MAP/microtubule affinity-regulating kinase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SOURCE FROM N.A.
RA Kahlina N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labber J., Lin Y.,
RA Pheasant M., Farmer A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL: BT007342; AAP36006.1; -.
DR HSP: Q63450.1A06
DR GO: GO:000524; F:ATP binding; IEA.
DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:Protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.

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DR InterPro: IPR001772; Kinase Cterm.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR001245; Tyr_kinase..
DR InterPro: IPR000449; UBA.
DR InterPro: IPR009060; UBA_like.
DR Pfam: PR02149; KAI; 1.
DR Pfam: PF00629; PKinase; 1.
DR Pfam: PF00627; UBA; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYR_Kc; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN_KINASE_STR; 1.
DR APP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 755 AA; 84332 MW; 493CD86CD3A4C06 CRC64;

Query Match          93.8%; Score 3504; DB 2; Length 755;
Best Local Similarity 91.4%; Pred. No. 4e-163;
Matches 690; Conservative 1; Mismatches 0; Indels 64; Gaps 3;

Qy      34 MINGRSATSDADQPHIGNYRLIKTGKGFAYKLABHILITGEVAVVKIIDTQNLSSS 93
Db      1 MINGRSATSDADQPHIGNYRLIKTGKGFAYKLABHILITGEVAVVKIIDTQNLSSS 60
Qy      94 LQKLFREVRIMKVLNHNINIKLFEVIEETKTLYLWMEYASGGEVFDLVAHGMRKEAR 153
Db      61 LQKLFREVRIMKVLNHNINIKLFEVIEETKTLYLWMEYASGGEVFDLVAHGMRKEAR 120
Qy      154 AKRQVSAVOYCHQKFIYHRDLKAENLLDADNMIIADPGFSNEFTFGNKLDTFCGSP 213
Db      121 AKRQIVSAVOYCHQKFIYHRDLKAENLLDADNMIIADPGFSNETFGNKLDTFCGSP 180
Qy      214 PYAPBELFOGKKTGDEGVNWSLGVILYTLVSSGLPFDGONLKELRARVLRGKRIIPFM 273
Db      181 PYAPBELFOGKKTGDEGVNWSLGVILYTLVSSGLPFDGONLKELRARVLRGKRIIPFM 240
Qy      274 STDCENLLKKFLILNPSKRGTLBOIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTTLMV 333
Db      241 STDCENLLKKFLILNPSKRGTLBOIMKDRMANNVGHEDDELKPYVEPLPDYKDPRTTLMV 300
Qy      334 SMGYTREELQDSLVGQRYNEVMATYLLGYKSSLEBDTITLKRPSADLTNSAPSPSH 393
Db      301 SMGYTREELQDSLVGQRYNEVMATYLLGYKSSLEBDTITLKRPSADLTNSAPSPSH 360
Qy      394 KVQRSVSNAPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKAASSTAKVP 452
Db      361 KVQRSVSNAPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEDDESGRKAASSTAKVP 420
Qy      453 PASPLPGLERKKTTPPTPSTNSVLTSTNRSRNSPLERASLGOASIQNGKD----- 503
Db      421 PASPLPGLERKKTTPPTPSTNSVLTSTNRSRNSPLERASLGOASIQNGKSLTWPGRAS 480
Qy      504 -----STAPQRYVVASPSAH 518
Db      481 STASASAAVSARPRQHKMSASVHPNKASGLPTESNCEVPRPSTAPQRYVVASPSAH 540
Qy      519 NISSSGAPDRITNPPRGVSSRSTFHAQQLROVRDQONLPYGVTPASPSGSGRRGASGS 578
Db      541 NISSSGAPDRITNPPRGVSSRSTFHAQQLROVRDQONLPYGVTPASPSGSGRRGASGS 600
Qy      579 IFSKFTSKFY-----RRNINPEBSKQDVEITLRPHVYVSGGNDKEKEPREAKRSIL 629
Db      601 IFSKFTSKFYRRNINPEBSKQDVEITLRPHVYVSGGNDKEKEPREAKRSIL 660
Qy      630 RFTWSMKTTSMEPNEMMREIRKVLNANSCOSELHEKYMILCMHGTGHDPIVQMEVCKL 689
Db      661 RFTWSMKTTSMEPNEMMREIRKVLNANSCOSELHEKYMILCMHGTGHDPIVQMEVCKL 720

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RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kozlyanski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: BC043730; AAH43730.1; -.
 DR HSP, P24941, 1010.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0004688; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001772; Kinase_Cterm.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI.1.
 DR Pfam: PF00069; Kinase.1.
 DR ProDom: PD000001; Prot_Kinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00165; UBA.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00106; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50030; UBA.1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 776 AA; 86805 MW; EC7EAD6C6362227 CRC64;

Query Match 85.5%; Score 3195.5; DB 2; Length 776;
 Best Local Simlarity 79.7%; Pred. No. 4,7e-148;
 Matches 620; Conservative 56; Mismatches 43; Indels 59; Gaps 6;

QY 3 SARTPLTNERBTOPTLGLDLSK-----SSKSNMGRNS-ATSDQPHIGNYRLK 57
 DB 2 TTRTLPFVERDADPALGHADOKTSSSGSSKPMKRCSTSTATTADDEPHIGNYRLK 61
 QY 58 TIGKGNPAKVKLARHILTGKEVAVKIIDKTOLNSSLOKLFREVRIMKVLNHPNIVLFE 117
 DB 62 TIGKGNPAKVKLARHVLTGKEVAVKIIDKTOLNSSLOKLFREVRIMKVLNHPNIVLFE 121
 QY 118 VITEKTLVIMVEYASGGEVFDYLVAGRMKEKEARKKFOVVSAYOYCHQKTIIVHDLK 177
 DB 122 VITEKTLVIMVEYASGGEVFDYLVAGRMKEKEARKKFOVVSAYOYCHQKTIIVHDLK 181
 QY 178 AENLLDADANNIKIADPGSENEFTFGNKLTFCGSPRYAAPLFOGKKYDGPEDVWSLG 237
 DB 182 AENLLDSDNNIKIADPGSENEFTFGNKLTFCGSPRYAAPLFOGKKYDGPEDVWSLG 241
 QY 238 VILYTVSGSLPFDGQNLKELRERVLKGYRIPIFYMSTDCENTLKKFLILNPSKRGTLGQ 297
 DB 242 VILYTVSGSLPFDGQNLKELRERVLKGYRIPIFYMSTDCENTLKKFLILNPSKRGTLGQ 301

QY 298 IMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELNVSMGYTREIOLSLVGORYNEWAT 357
 DB 302 IMKDRMNVGHEDDELKPYVEPLPDYKDPRTTELNVSMGYTREIOLSLVGORYNEWAT 361
 QY 358 YLLLGYSSELEDDITTLKRPASADITNSGAPSPSHKVQSVANPKQRFSDQAGPAIP 417
 DB 362 YLLGRTSEMDDNLTILKRPPEPDISNSIVTSPAHKVQSVANPKQRLSDQAGPAIP 421
 QY 418 TSNYSKKTOSNNAENKRPREDRESGRKASTLKVASPLPGLEKKTTPPTNSVLST 477
 DB 422 NSNSYSKKTOSNNAENKRPREDRESGRKASTLKVASPLPGLEKKTTPPTNSVLST 481
 QY 478 STNRSSNPLTERASISQASISONGK----- 503
 DB 482 GTRSRSPMLDPSLVPVSGVNGKSFSTPGSRASTASAPATSARIQOKMSNVSHP 541
 QY 504 -----STAPQRPVVASPSAHNISSGAGADRTNPPRGVSSRSTFPAQOL 547
 DB 542 SKPAPSELCNCDVQRPSTAPQRPVVASPSAHNISSGAGADRTNPPRGVSSRSTFPAQOL 599
 QY 548 RQVRDQONLPG-VTPASPSGHSQGRGASGSIIFSFTSKFTFRNLNBPESKORVETLRP 606
 DB 600 RQVRDQONLPG-VTPASPSGHSQGRGASGSIIFSFTSKFTFRNLNBPESKORVETLRP 659
 QY 607 HVGSGSGNDKEKEPEPEAKRSLRFTWMSKTTSSMBENEMMRIRKVLNANSCOSELHEK 666
 DB 660 H-LSYVDKEDKDHDSKRSRLFTWMSKTTSSMBENEMMRIRKVLNANSCOSELHEK 718
 QY 667 YMLLCMCHGTGPHEDPFVOMEWCKLPRLSLNGVRFKRSIGTSNAFKNIASKINIELTL 724
 DB 719 YMLLCMCHGTGPHEDPFVOMEWCKLPRLSLNGVRFKRSIGTSNAFKNIASKINIELTL 776

RESULT 11
 Q8QGV3 PRELIMINARY; PRT; 785 AA.
 ID 08QGV3;
 AC 08QGV3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Serine/threonine kinase.
 GN Name=MARK2;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RA Nakajo N., Shimuta K., Uto K., Sagata N.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AB071963; BAB86594.1; -.
 DR HSP, P24941, 1010.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0004688; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001772; Kinase_Cterm.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF02149; KAI.1.
 DR Pfam: PF00069; Kinase.1.
 DR ProDom: PD000001; Prot_Kinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00165; UBA.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50030; UBA; 1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 785 AA; 87949 MW; D56FBI82033EC64; CXC64;
 Query Match
 Best local similarity 78.9%; Pred. No. 1,1e-147;
 Matches 621; Conservative 56; Mismatches 42; Indels 68; Gaps 7;
 QY 3 SARPLTLNLRDTEOPLTGLHLSKPS---SSKSNMIRGNS-ATSDDEPHIGNYLLK 57
 DB 2 TTRPLPLTVNERDADQALGHADOKTSSGSSSKSNMRCRTSIATTADEPHIGNYLLK 61
 QY 58 TIGGNPAKYLAHHITLTKGKAVAKIIDKTQNLNSSLQKLFREVRIMKVLNHPNIVLFE 117
 DB 62 TIGGNPAKYLAHHITLTKGKAVAKIIDKTQNLNSSLQKLFREVRIMKVLNHPNIVLFE 121
 QY 118 VIETKTLVLYMEVYASGGEVFDVLAHGRMKEKARAFQVYSAVOYCHQKFIYHRLK 177
 DB 122 VIETKTLVLYMEVYASGGEVFDVLAHGRMKEKARAFQVYSAVOYCHQKFIYHRLK 181
 QY 178 AENILLADAMNLIKADFGSNEFTFGNKLDTFCGSPPYAAPLFGKKYDGPEDVWSLG 237
 DB 182 AENILLADSDMNLIKADFGSNEFTFGNKLDTFCGSPPYAAPLFGKKYDGPEDVWSLG 241
 QY 238 VIITVTVSGSLPFGQULKEIRERVLRGKTRIPYMSIDENILKKFLINPSKRGTLQ 297
 DB 242 VIITVTVSGSLPFGQULKEIRERVLRGKTRIPYMSIDENILKKFLINPSKRGTLQ 301
 QY 298 IMDRMNVVGHEDDELKPYVEPLPDYDQPRTELMVSMGYRREIIDSILVQGRYNEVMAT 357
 DB 302 IMDRMNVVGHEDDELKPYVEPLPDYDQPRTELMVSMGYRREIIDSILVQGRYNEVMAT 361
 QY 358 YLLGYSSSLLEGITTLKRPSPADLTNSSAPSHVQSVSVANPQORFSPQAGPAIP 417
 DB 362 YLLGYSSSLLEGITTLKRPSPADLTNSSAPSHVQSVSVANPQORFSPQAGPAIP 421
 QY 418 TSNYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLS 477
 DB 422 TSNYSKKTOSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLS 481
 QY 478 STNRSNRPILLERASLGQASIQNGKD----- 503
 DB 482 STNRSNRPILLERASLGQASIQNGKD----- 511
 QY 504 -----STAPQRYVVASPSAHNITSSSGAGADRTNPRGVSSRSTFPAQOL 547
 DB 542 SKPAPSLIEGNCVQRPSTAPQRYVVASPSAHNITSSSGAGADRTNPRGVSSRSTFPAQOL 599
 QY 548 ROYVDOQNLPLFG-VTPASPSGHSQGRGAGSIFSKFTSKFVRNL-----NEPS 597
 DB 600 ROYVDOQNLPLFG-VTPASPSGHSQGRGAGSIFSKFTSKFVRNL-----NEPS 659
 QY 598 KDRVETLRPHVVGSGGNDKEKEEFREKPSLRFTWSMKTSSMEBENMREIRKVLN 657
 DB 660 KDRVETLRPHVVGSGGNDKEKEEFREKPSLRFTWSMKTSSMEBENMREIRKVLN 718
 QY 658 SCQSELEHEKYMILCMGTBPHEDFVQWEMEVCLPRLSLNGVRFKRLISGSAFKIATK 717
 DB 719 NCHEGSEKYMILCMGTBPHEDFVQWEMEVCLPRLSLNGVRFKRLISGSAFKIATK 778
 QY 718 IANELKL 724
 DB 779 IANELKL 785
 RESULT 12
 Q804T1 PRELIMINARY; PRT; 780 AA.
 AC Q804T1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Ser/Thr protein kinase PAR-1B alpha.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ossipova O., He X., Green U.;
 RT "Molecular cloning and developmental expression of Par-1/MARK
 homologues Xpar-1A and Xpar-1B from Xenopus laevis";
 RL Gene Expr. Patterns 2:145-150(2002).
 CC -1- Similarity: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF509738; AAC27568.1; -.
 DR HSP; P24941; 1010.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011772; Kinase_Cterm.
 DR InterPro; IPR011009; Kinase_Like.
 DR InterPro; IPR00719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR000449; UBA.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; PKinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50030; UBA; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 780 AA; 86957 MW; EABA9DA4B64DC41 CRC64;
 Query Match
 Best local similarity 81.0%; Score 3027; DB 2; Length 780;
 Matches 593; Conservative 56; Mismatches 61; Indels 58; Gaps 6;
 QY 11 INERDTEOPLTGLHLSKPS---KSNMIRGNS-ATSDDEPHIGNYLLKTIKGNPAK 66
 DB 17 INPLAHPBALGHADPKTSSSKSNMRCRTSIATTADEPHIGNYLLKTIKGNPAK 76
 QY 67 VGLAHHITLTKGKAVAKIIDKTQNLNSSLQKLFREVRIMKVLNHPNIVLFEVLETETLY 126
 DB 77 VGLAHHITLTKGKAVAKIIDKTQNLNSSLQKLFREVRIMKVLNHPNIVLFEVLETETLY 136
 QY 127 LVMEVYASGGEVFDVLAHGRMKEKARAFQVYSAVOYCHQKFIYHRLKAEINILLAD 186
 DB 137 LVMEVYASGGEVFDVLAHGRMKEKARAFQVYSAVOYCHQKFIYHRLKAEINILLAD 196
 QY 187 MNIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFGKKYDGPEDVWSLGVIITVTVSG 246
 DB 197 MNIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFGKKYDGPEDVWSLGVIITVTVSG 256
 QY 247 SLPLFGQULKEIRERVLRGKTRIPYMSIDENILKKFLINPSKRGTLQIMDRMNV 306
 DB 257 SLPLFGQULKEIRERVLRGKTRIPYMSIDENILKKFLINPSKRGTLQIMDRMNV 316
 QY 307 GHEDELKPYVEPLPDYDQPRTELMVSMGYRREIIDSILVQGRYNEVMATYLLGYSS 366
 DB 317 GHEDELKPYVEPLPDYDQPRTELMVSMGYRREIIDSILVQGRYNEVMATYLLGYSS 376
 QY 367 ELEGDITLKPSPADLTNSSAPSHVQSVANPQORFSPQAGPAIPTSNSYSKKT 426
 DB 377 EMDNDHLTKRPPRGVSNNTVSSPAHNVQSVANPQORFSPQAGPAIPTSNSYSKKT 436
 QY 427 OSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSSTNRSNP 486
 DB 437 OSNNAENKRPEDRESGRKASTAKVPASPLPGLERKKTPTPTSTNSVLSSTNRSNP 496

QY 487 LLEBASIGQASIONGKD----- 503
: : : : :
Db 497 MLDRATLVPSIINXKGSFWMPSGRASTASAPATARIHQKSMSTSVHPSKAPSLDG 556
QY 504 -----STPQRYVPAVPSAHNITSSGGAAPDRTPNPRGVSSNSTFHAGLRQVQDQNTL 556
: : : : :
Db 557 NCDVORASTAPORLPVSPSAHNITSSA-ATERNNPRGVSSNSTFHAGVQRQARDQNTL 614
QY 557 PYGVTPSPSGHGRGASGSITFSKFTSKFVRNINLEPESKDRVETLPRPHVVGSSGNDK 616
: : : : :
Db 615 GF-VSPSPSGISQGRGATGSIPTSKTSKFKVRKNPDPEKORVESTTRPH-LSVDKEK 672
QY 617 EKEEFPAKPSRLFTWSMKTSSMEPNEMAREIRKVLNDANSQSELEHEKMLCMHGT 676
: : : : :
Db 673 DKEDLADSKPSRLFTWSMKTSSMEPNEMISEICVKLDANNCQYESODKTMILCVHGT 732
QY 677 GHEDPVQWEMEVCCLPRLSLNGVRFKRIISGTSMAFKNIASKIANELKL 724
: : : : :
Db 733 GHNVYQWEMEVCCLPRLSLNGVRFKRIISGTSIAFKNIASKIANDELKL 780
RESULT 13
QYVHUS PRELIMINARY; PRT; 795 AA.
ID QYVHUS;
AC QYVHUS;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eukl motif serine-threonine protein kinase 3.
GN Name=mark1; Synonym=Emk3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Darnon Y.M., Le Morvan V.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF453686; AAL50826.1; -.
DR HSSP; P24941; IOIO.
DR MGI; MGI:2664902; Mark1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00669; PKinase; 1.
DR Pfam; PF00627; UBA; 1.
DR ProDom; PD000001; Proc_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00300; UBA; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 795 AA; 88545 MW; 79A74E2EEB9A35A2 CRC64;
Query Match 68.5%; Score 2561; DB 2; Length 795;
Boot local similarity 65.6%; Pred. No. 4.6e-117;
Matches 528; Conservative 81; Mismatches 102; Indels 94; Gaps 15;
QY 3 SARTPLPTLNERDTEOPTL--GHLD-----SKPSKSNMIRGNASATSA-DEOPHIGNRV 54
: : : : :
Db 2 SARTPLPTVNERDTEHNTSVDTERTHPTKSSRNIRCRNISTSATDEQPHIGNRV 61
QY 55 LKLTIGKSNPAKTKLARHILITGKEVAVKIIDTKQLNSSSLQKLPREVRINKVLNHPYIK 114
: : : : :
Db 62 LQRTIGKGNPAKTKLARHVLITGRBVAVKIIDTKQLNPTSLQKLPREVRINKVLNHPYIK 121
QY 115 LPEVIEETKTLVLMVEYASGGEVFDVLVAHGRMKEKARAKFRQVNSAVQYCHQKFLVHR 174

Db 122 LPEVIEETKTLVLMVEYASGGEVFDVLVAHGRMKEKARAKFRQVNSAVQYCHQKFLVHR 181
QY 175 DLKAENILDLADNMNITKIDFGFSENEFTFGKLDTPFGSGPPYAADELFGKKYDGEVDVW 234
Db 182 DLKAENILDLADNMNITKIDFGFSENEFTFGKLDTPFGSGPPYAADELFGKKYDGEVDVW 241
QY 235 SLGVILYTLVSGSLPDQGLKELRERVLRGKTRIPYMSITDDELKKLLINPSKGT 294
: : : : :
Db 242 SLGVILYTLVSGSLPDQGLKELRERVLRGKTRIPYMSITDDELKKLLINPSKGT 301
QY 295 LEQIMKDRMNVNHEDELKPYVEPLPDYKDPRTTELIMVSMGYTRERISQSLVQORYNEV 354
Db 302 LEQIMKDRMNVNHEDELKPYSEPELDLNDAGRIDIMWTMGARDEINDALVSQKDEV 361
QY 355 MATYLLIGYKSSLEGG-----DTTLKPPPSADLTNSASPSPH-KVQSVSANPKQR 407
: : : : :
Db 362 MATYLLIGRKPPEFEGESLISGNLCORSRPSDLNNSTLQSPAHLLKVGRSISANQQR 421
QY 408 FSDQAGPAITPSNSYSKKTQSNNAENKRPPE-DREGSKASST-----AKVPASPPLGLE 461
: : : : :
Db 422 FSDHAGPSLPPAVSYTKRPQANSVESEQKEWDKOTARRLGSTVGSKSEVTASPLVGP 481
QY 462 RKKTPTPTSTNSVLTSTYNRSRNSPLLERASLQASIONGKST----- 505
: : : : :
Db 482 RKGSTASPS-NVYSGSGMAKRTTYCERSTDYKALQNGRDSLTMSGASSMSAGSTV 540
QY 506 -----APQRPVAPSAHNITSSGGA 526
Db 541 ASAGPAPRPHQKSMSTSGHPIKVTLPTIKDGEAVRPGAQGVPAASPSAHISAS--T 598
QY 527 PDRTPNPRGVSSNSTFHAGLRQVDOQNTPYGVTPASPSGSGGQ-----RRASGSI 581
: : : : :
Db 599 PDRTPNPRGVSSNSTFHAGLRQVDOQNTPYGVTPASPSGSGGQ-----RRASGSI 654
QY 582 KFTSKFVRNINLEPESKDRVETLPRPHVVGSGGNDKE--KEEFPAKPSRLFTWSMKTSS 639
: : : : :
Db 655 KITSKVRNDRPSRGEASGRDTPAR-----GSSGPKRDEEGEAPRSLRFTWSMKTSS 710
QY 640 SMEPNEMAREIRKVLNDANSQSELEHEKMLCMHGTGPHEDPVQWEMEVCCLPRLSLNGV 699
Db 711 SMDPNMLEIRKVLNDANTCDVEQKERFLLFCVHGDAQSIVQWEMEVCCLPRLSLNGV 770
QY 700 RFRKRIISGTSMAFKNIASKIANELKL 724
Db 771 RFRKRIISGTSIAFKNIASKIANDELKL 795
RESULT 14
ID QYVHUS PRELIMINARY; PRT; 793 AA.
AC QYVHUS;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine kinase.
GN Name=mark1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Drewes G., Ebneeth A., Preuss U., Mandelkow E., Mandelkow E.;
RT "MARK - a Novel Family of Protein Kinases that Phosphorylate
Microtubule-associated Proteins and Trigger Microtubule Disruption.";
Cell 89:297-308(1997).
RL EMBL; Z63868; CAB06294.1; -.
DR HSSP; P24941; IOIO.
DR GO; GO:0005524; F:ATP binding; IEA.

DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO:0016740; F:transferase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011772; Kinase_Cterm.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR00719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI; 1.
 DR Pfam: PF00069; PKinase; 1.
 DR Pfam: PF00627; UBA; 1.
 DR Prodom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00030; UBA; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 793 AA; 88234 MW; C5BCAC0BB9A0A3 CRC64;

Query Match 68.4%; Score 2555; DB 2; Length 793;
 Best Local Similarity 65.5%; Pred. No. 9e-117;
 Matches 525; Conservative 82; Mismatches 105; Indels 90; Gaps 14;

3 SARTPLPTLNERTDEPTL--GHLD-----SKPSSKNNIRGNSTSA-DEQPHIGNR 54
 2 SARTPLPTVNERTDENTSVDTGETHPTPTSSSRQNI PRCONSITSADEQPHIGNR 61

55 LKTTGKGNPAKYLARHILITGKEVAVKIIDKTQUNSSLOLFRFVRIMKVLNHPNIYK 114
 62 LKTTGKGNPAKYLARHILITGKEVAVKIIDKTQUNSSLOLFRFVRIMKVLNHPNIYK 121

115 LFEVTEKTLTYLMEYASGGEVFDYLAHGRMKEKARAKFRQVSAVOYCHOKETIVHR 174
 122 LFEVTEKTLTYLMEYASGGEVFDYLAHGRMKEKARAKFRQVSAVOYCHOKETIVHR 181

175 DLKAEMLLDADNNIKIADFGFSGNEFTFGNKLDTFCGSPYAPABELFOGKKYDGPEDVW 234
 182 DLKAEMLLDADNNIKIADFGFSGNEFTFGNKLDTFCGSPYAPABELFOGKKYDGPEDVW 241

235 SLGVTITVYSGSLPRPGONKELREVLGKRIIPYMSDGCNLLKFFLIINPSKRG 294
 242 SLGVTITVYSGSLPRPGONKELREVLGKRIIPYMSDGCNLLKFFLIINPSKRG 301

295 LEQIMKRMWNVGHEDELKPYVEPLDYPDKPRTELMVSGYTRREIODSLVGQRYNEV 354
 302 LEQIMKRMWNVGHEDELKPYVEPLDYPDKPRTELMVSGYTRREIODSLVGQRYNEV 361

355 MATYLLIGYKSSLEAG-----DITTLKPRPSALUTSSAPSPH-KVORSVSANPRQR 407
 362 MATYLLIGYKSSLEAG-----DITTLKPRPSALUTSSAPSPH-KVORSVSANPRQR 421

408 FSDQGPALIPNSNSKKTOSNNAKRPEE-DRESGKASST-----AKVPASPLPGL 461
 422 FSDHGPESIPPAVSTTKRPAQNSVSEKEMWDKDTARLGSTTVGSGSEVTAPLVPD 481

462 RKTTPTSTNSVLTSTNRSNPLERASLQASLQNGKDS-----504
 482 RKSSAGPS-NNVVSGGSMTRNTYVCRSTDRYALQNGRDSLITWSSASMSGSTV 540

505 -----TAP-----ORVPVASSAHNISSGGA 526
 541 ASAGSAPRHRQKSMSTSGHPIKVTLPITTKGSEAYRPGTAKORVPASPSAHNISAS--T 598

527 PDRTNPGRGVSRSSTFHAGQLQVADQNLPGYVTPASPS-----GHSQGRGASGISFSK 582
 599 PDRTPFGSSSRSTFHGEQL---RHRSAVSGPPASPSHDYALAHARAGTSGITISK 655

583 FTSKFRNLNLPESKDRVETLRPHVVGSGNDKEKEPRKAPSLSLFTSMKTTSSME 642
 656 ITSKEVRBDPSEGEASGRITDAR---GSSGEPKDEKGEKAPRSISLFTWSMKTSSMD 711

Qy 643 PNEMRIRKYLNDANSQSELEHKYMLCMHGTPGHEDFYQWEMEVCKLPRLSLNGVRFK 702
 Db 712 PNDVREIRKYLNDNTDQYREKRFLLVCVHGADARQDSLVOYEMEVCKLPRLSLNGVRFK 771

Qy 703 RISGTSMAFKNIASKINELKL 724
 Db 772 RISGTSIAFKNIASKINELKL 793

RESULT 15
 ID 09POL2 PRELIMINARY; PRT; 795 AA.
 AC 09POL2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MARK.
 GN Name=MARK;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Zhou H.J., Huang X.W., Zhou Y., Hu S.L., Yuan J.G., Qiang B.Q.,
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF154845; AAF72103.1; -.
 DR HSPB; P24941; 1010.
 DR Genew; HGNC:6896; MARK1.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO:0016740; F:transferase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011772; Kinase_Cterm.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR00719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAI; 1.
 DR Pfam: PF00069; PKinase; 1.
 DR Prodom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 795 AA; 88966 MW; 89C9ABF265D679CB CRC64;

Query Match 68.1%; Score 2546; DB 2; Length 795;
 Best Local Similarity 65.1%; Pred. No. 2.5e-116;
 Matches 524; Conservative 82; Mismatches 105; Indels 94; Gaps 16;

3 SARTPLPTLNERTDEPTL--GHLD-----SKPSSKNNIRGNSTSA-DEQPHIGNR 54
 2 SARTPLPTVNERTDENTSVDTGETHPTPTSSSRQNI PRCONSITSADEQPHIGNR 61

115 LKTTGKGNPAKYLARHILITGKEVAVKIIDKTQUNSSLOLFRFVRIMKVLNHPNIYK 174
 122 LFEVTEKTLTYLMEYASGGEVFDYLAHGRMKEKARAKFRQVSAVOYCHOKETIVHR 181

175 DLKAEMLLDADNNIKIADFGFSGNEFTFGNKLDTFCGSPYAPABELFOGKKYDGPEDVW 234
 182 DLKAEMLLDADNNIKIADFGFSGNEFTFGNKLDTFCGSPYAPABELFOGKKYDGPEDVW 241

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